

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:34:33 ; Search time 32.39 Seconds
(without alignments)
256.730 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQPGAEVLKPGTSLVSL.....DGWDYADYWGQTSVTVS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:**

1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	533.5	81.1	120	2	B22769		Ig heavy chain V r
2	527.5	80.2	120	2	S41394		Ig heavy chain V r
3	519.5	79.0	116	2	S53751		antibody Fab Jel 1
4	516	78.4	138	2	E32513		Ig heavy chain pre
5	515	78.3	123	2	S20646		Ig heavy chain pre
6	514.5	78.2	139	1	MHMS18		Ig heavy chain pre
7	514.5	78.2	287	4	PC4402		peB leader/Ig hea
8	514	78.1	120	2	S25175		Ig heavy chain V r
9	507.5	77.1	141	2	JL0076		Ig heavy chain pre
10	507	77.1	122	2	S20643		Ig heavy chain pre
11	499.5	75.9	117	2	B27563		Ig heavy chain V r
12	498.5	75.8	118	2	C30560		Ig heavy chain V r
13	495	75.2	131	2	A27472		Ig heavy chain pre
14	495	75.2	246	2	S38950		Ig gamma chain - m
15	495	75.2	446	2	S40295		Ig gamma-2a chain
16	492.5	74.8	135	2	A30577		Ig heavy chain pre
17	492.5	74.8	139	2	PS0024		Ig heavy chain pre
18	491.5	74.7	122	2	S24287		Ig heavy chain V r
19	489	74.3	110	2	S26137		Ig gamma chain V r
20	488.5	74.2	126	2	S31930		Ig heavy chain pre
21	487	74.0	136	2	PL0208		Ig heavy chain pre
22	486.5	73.9	131	2	S66537		Ig heavy chain V r
23	484.5	73.6	113	2	S25041		Ig heavy chain V r
24	483.5	73.5	115	2	C27563		Ig heavy chain V r
25	483.5	73.5	136	2	JL0077		Ig heavy chain V r
26	482	73.3	116	2	S55422		Ig heavy chain pre
27	481	73.1	117	2	G45722		Ig heavy chain V r
28	479.5	72.9	120	1	MHMS15		anti-glycoprotein
29	478	72.6	138	1	HVMST7		Ig heavy chain pre

30 477.5 72.6 111 2 S25048 Ig heavy chain V r
31 477.5 72.6 113 2 S25044 Ig heavy chain V r
32 477 72.5 98 2 PH1160 Ig heavy chain V r
33 476 72.3 136 2 B47159 Ig heavy chain V r
34 475.5 72.3 111 2 S25052 Ig heavy chain V r
35 474 72.0 121 2 A26405 Ig heavy chain V r
36 473.5 72.0 137 2 F29380 Ig heavy chain pre
37 473 71.9 119 2 C30582 Ig heavy chain V-D
38 473 71.9 123 2 E48677 Ig heavy chain V r
39 472.5 71.8 111 2 S25047 Ig heavy chain V r
40 472.5 71.8 120 2 S25024 Ig heavy chain V r
41 472.5 71.8 120 2 S09956 Ig heavy chain V-D
42 472 71.7 119 2 PL0089 Ig heavy chain V r
43 471.5 71.7 111 2 S25032 Ig heavy chain V r
44 471.5 71.7 111 2 S25055 Ig heavy chain V r
45 470.5 71.5 116 2 S26309 Ig heavy chain V r

ALIGNMENTS

RESULT 1
B22769
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Dillardrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982.
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236036
A:Accession: B22769
A:Molecule type: protein
A:Residues: 1-120 <DIL>
A:Note: peptides and unsequenced residues were positioned by homology with the B1-8
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 533.5; DB 2; Length 120;
Best Local Similarity 84.3%; Pred. No. 6.5e-40;
Matches 102; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
QY 1 QVQLQPGAEVLKPGTSLVSLCKSGYGYTFTSYMHVVKORPGQGLEWIGEDIPSPSTNTY 60
|||||
Db 1 QVQLQPGAEVLKPGASVKVSKASGYTFTSYMHVVKORPGQGLEWIGRIHPSDSDTNY 60
QY 61 NOKFKGKATLTVDISSTAYMQLSLTSDSAVYYCARGYDGDYADYWGQTSVTVS 120
|||||
Db 61 NOKFKGKATLTVDKPSSTAYMQLSLTSDSAVYYCARYDYGYSSY-FDYWGQGTTLTVS 119
QY 121 S 121
Db 120 S 120

RESULT 2
S41394
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S41394
R:Margatite, C.; Gilbert, D.; Brard, F.; Tron, F.
submitted to the EMBL Data Library, January 1994
A:Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti
A:Reference number: S41393
A:Accession: S41394
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAR>
A:Cross-references: EMBL:229586; NID:9452354; PIDN:CAA82703.1; PID:g1334080

A:Molecule type: DNA
A:Residues: 1-117 <1862>
A:Note: the BI-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten
A:Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R:DilDrop, R.: Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026
A:Accession: A22769
A:Molecule type: protein
A:Residues: 20-139 <DI1>
A:Note: the V region of the BI-8 delta chain, derived as a spontaneous class switch variant
of the mu chain
C:Genetics:
A:Introns: 16/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence
F:20-139/Product: Ig kappa chain V region (BI-8) #status experimental <MAT>
F:34-117/Domain: immunoglobulin homology
F:118-124/Region: D segment
F:125-139/Region: J segment (JH2)

Sat Apr 14 08:10:30 2001

us-08-700-737-9.rpr

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Db 80 NEKEKATLTVDKPSSTAYMQLSSLTSEDSAVVYCAREGPAG-----DYWGQGTTLTVS 134
QY 121 S 121
Db 135 S 135

RESULT 10
S20643
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20643
R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A:Reference number: S20639
A:Accession: S20643
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <LOS>
A:Cross-references: EMBL:X6498; NID:g52606; PIDN:CAA46131.1; PID:g52607
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 507; DB 2; Length 122;
Best Local Similarity 80.6%; Pred. No. 1.3e-37;
Matches 100; Conservative 6; Mismatches 12; Indels 6; Gaps 2;

QY 1 QVLOQPGAEVLKPGTSTVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNY 60
||||| ||||||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Db 1 QVLOQXXGAELVKPGASVKLSCKASGYTFIRYIHWKQRPQGLEWIGEDIPSDNYTY 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

QY 61 NOKFKGKATLTVDISSTAYMQLSSLTSEDSAVVYCAARGYDGMW----YADYWGQGT 116
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 61 NOKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVVYCARREY--YDLRRGHANDYWGQGT 118

QY 117 VTVS 120
|||||
Db 119 VTVS 122

RESULT 11
B27563
Ig heavy chain V region (T14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 23-Jul-1999
C:Accession: B27563
R:Carmack, C.E.; Pincus, S.H.
J. Immunol. 137, 3983-3989, 1986
A:Title: Variable regions of antibodies to synthetic polypeptides. II. Analysis of varia
A:Reference number: A92812; MUID:87059009
A:Accession: B27563
A:Molecule type: DNA
A:Residues: 1-117 <CAR>
A:Cross-references: GB:M14974; NID:g195260; PIDN:AAA38226.1; PID:g195261
A:Note: this sequence was determined from the differentiated gene
A:Note: the authors translated the codon GGT for residue 54 as Ala and TAC for residue 5
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-95/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 499.5; DB 2; Length 117;
Best Local Similarity 78.8%; Pred. No. 5.8e-37;
Matches 93; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 4 LOQPGAEVLKPGTSTVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNYNQK 63
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 4 LOQPGAEVLKPGASVKLSCKASGYTFTNYIHWKQRPGRGLEWIGRIDPNSSGGTKYNEK 60

QY 64 FKKGATLTVDISSTAYMQLSSLTSEDSAVVYCAARGYDGMWYADYWGQGTSTVTSS 121
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 61 FKNKATLTINKPNTAYMQLSSLTSDSAVYCAR-GYDYSYAMDYWGQGTSTVTSS 117

RESULT 12
C30560
Ig heavy chain V region (35.8.2H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C:Accession: C30560
R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono
A:Reference number: A30560; MUID:89110062
A:Accession: C30560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <MAT>
A:Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 498.5; DB 2; Length 118;
Best Local Similarity 80.2%; Pred. No. 7.2e-37;
Matches 97; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVLOQPGAEVLKPGTSTVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNY 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 1 QVHLQSGAEVLKPGASVKISCKASGYTFTSYWMHWKORPGOGLEWIGEDIPSNYTN 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

QY 61 NOKFKGKATLTVDISSTAYMQLSSLTSEDSAVVYCAARGYDGMWYADYWGQGTSTVTS 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 61 NOKFKNKATLTVDKSSNTAYMQLSSLTSEDSAVVYCARWGTSW---PAYWGQGTTLTVS 117

QY 121 S 121
Db 118 A 118

RESULT 13
A27472
Ig heavy chain precursor V region (IE9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 18-Oct-1996
C:Accession: A27472
R:Liu, A.Y.; Mack, P.W.; Champion, C.I.; Robinson, R.R.
Gene 54, 33-40, 1987
A:Title: Expression of mouse::human immunoglobulin heavy-chain cDNA in lymphoid cells
A:Reference number: A27472; MUID:87277430
A:Accession: A27472
A:Molecule type: mRNA
A:Residues: 1-131 <LIU>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:5-54/Region: complementarity-determining 1
F:20-131/Product: Ig heavy chain V region IE9 #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:69-85/Region: complementarity-determining 2
F:118-125/Region: complementarity-determining 3

Query Match 75.2%; Score 495; DB 2; Length 131;
Best Local Similarity 82.6%; Pred. No. 1.6e-36;
Matches 95; Conservative 3; Mismatches 13; Indels 4; Gaps 2;

QY 1 QVLOQPGAEVLKPGTSTVKLSCKGKGYGTYFTSYWMHWKORPGOGLEWIGEDIPSESNY 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Db 20 QVLOQPGAEVLKPGASVKLSCKASGYTFTSYWMHWKORPGOGLEWIGEDIPSNGRNTY 79
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:35:47 ; Search time 21.32 Seconds
(without alignments)
194,414 Million cell updates/sec

Title: US-08-700-737-9

Perfect score: 658

Sequence: 1 QVQLQPCAEIVKPGTSVKL.....DGWDYADYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	514.5	78.2	139	1	HV07_MOUSE	P01751	mus musculus
2	479.5	72.9	120	1	HV50_MOUSE	P06329	mus musculus
3	478	72.6	138	1	HV48_MOUSE	P03980	mus musculus
4	469.5	71.4	137	1	HV11_MOUSE	P01755	mus musculus
5	469	71.3	140	1	HV02_MOUSE	P01746	mus musculus
6	468	71.1	120	1	HV03_MOUSE	P01747	mus musculus
7	464	70.5	117	1	HV06_MOUSE	P01750	mus musculus
8	452	68.7	117	1	HV09_MOUSE	P01753	mus musculus
9	451	68.5	117	1	HV05_MOUSE	P01749	mus musculus
10	447	67.9	117	1	HV12_MOUSE	P01756	mus musculus
11	447	67.9	121	1	HV01_MOUSE	P01745	mus musculus
12	445	67.6	117	1	HV04_MOUSE	P01748	mus musculus
13	445	67.6	117	1	HV13_MOUSE	P01757	mus musculus
14	441.5	67.1	118	1	HV51_MOUSE	P06330	mus musculus
15	441	67.0	117	1	HV49_MOUSE	P01754	mus musculus
16	440	66.9	117	1	HV10_MOUSE	P01758	mus musculus
17	409	62.2	136	1	HV15_MOUSE	P01759	mus musculus
18	395	60.0	117	1	HV52_MOUSE	P06327	mus musculus
19	383	58.2	117	1	HV14_MOUSE	P01758	mus musculus
20	372.5	56.6	147	1	HV1C_HUMAN	P01743	homo sapien
21	365	55.5	117	1	HV1B_HUMAN	P23083	homo sapien
22	357	54.3	117	1	HV1G_HUMAN	P01812	mus musculus
23	348	52.9	117	1	HV42_MOUSE	P01808	mus musculus
24	347.5	52.8	114	1	HV00_MOUSE	P01741	mus musculus
25	341.5	51.9	119	1	HV38_MOUSE	P01807	mus musculus
26	335	50.9	117	1	HV41_MOUSE	P01811	mus musculus
27	333.5	50.7	119	1	HV37_MOUSE	P01805	rattus norv
28	328	49.8	142	1	HV01_RAT	P01809	mus musculus
29	327	49.7	118	1	HV39_MOUSE	P01783	mus musculus
30	326.5	49.6	136	1	HV16_MOUSE	P01810	mus musculus
31	325.5	49.5	119	1	HV40_MOUSE	P06331	homo sapien
32	325.5	49.5	146	1	HV21_HUMAN	P01771	homo sapien
33	319	48.5	121	1	HV33_HUMAN		

34	316	48.0	125	1	HV1F_HUMAN	P06326	homo sapien
35	312	47.4	117	1	HV1A_HUMAN	P01742	homo sapien
36	311.5	47.3	122	1	HV3G_MOUSE	P01768	homo sapien
37	308	46.8	115	1	HV32_MOUSE	P01801	mus musculus
38	306.5	46.6	126	1	HV3K_HUMAN	P01772	homo sapien
39	306	46.5	113	1	HV30_MOUSE	P01799	mus musculus
40	305.5	46.4	120	1	HV1H_HUMAN	P80421	homo sapien
41	303.5	46.1	124	1	HV1D_HUMAN	P01760	homo sapien
42	302.5	46.0	111	1	HV35_MOUSE	P01804	mus musculus
43	301	45.7	113	1	HV27_MOUSE	P01796	mus musculus
44	301	45.7	123	1	HV25_MOUSE	P01794	mus musculus
45	300	45.6	115	1	HV33_MOUSE	P01802	mus musculus

ALIGNMENTS

```
RESULT 1
HV07_MOUSE
ID AC HV07_MOUSE STANDARD; PRT; 139 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC InterPro; IPR003006; -
CC Pfam; PF00047; ig; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC DOMAIN 20 49 FRAMEWORK 1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
CC DOMAIN 55 68 FRAMEWORK 2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
CC DOMAIN 86 117 FRAMEWORK 3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 139 139
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
```

Query Match 78.2%; Score 514.5; DB 1; Length 139;
Best Local Similarity 81.0%; Pred. No. 1e-44;
Matches 98; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

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QY 1 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYWVHWKQRPQGLEWIGTIDPSESNTNY 60
DB 20 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYWVHWKQRPQGLEWIGTIDPSESNTNY 79
QY 61 NOKFKGKATLVDTSSSTAYMQLSLTSDSAVYVCARGGYDGMWDAIDYWGQGTSTVTS 120
DB 80 NEKFKSKATLVDTKSSSTAYMQLSLTSDSAVYVCARYDYGGSSY-FDYWGQGTSTVTS 138
QY 121 S 121
DB 139 S 139
RESULT 2
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=841182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;
Query Match 72.6%; Score 478; DB 1; Length 138;
Best Local Similarity 74.6%; Pred. No. 4.4e-41;
Matches 91; Conservative 11; Mismatches 16; Indels 4; Gaps 2;
QY 1 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYWVHWKQRPQGLEWIGTIDPSESNTNY 60
DB 20 QVLOQPGAEVLKPGTGVKLSCKGKGYGTYFTSYWVHWKQRPQGLEWIGTIDPSESNTNY 79
QY 61 NOKFKGKATLVDTSSSTAYMQLSLTSDSAVYVCARGGYDGMWDAIDYWGQGTSTVTS 119
DB 80 NEKFKSKATLVDTKSSSTAYMQLSLTSDSAVYVCARYDYGGSSY-FDYWGQGTSTVTS 136
QY 120 SS 121
DB 137 SA 138
RESULT 4
HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC EMBL: J00539: AAA38172.1; -
DR PIR: A02038: G2MS43.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;
```

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Query Match 71.4%; Score 469.5; DB 1; Length 137;
Best Local Similarity 73.4%; Pred. No. 3.1e-40;
Matches 91; Conservative 7; Mismatches 17; Indels 9; Gaps 2;

QY 1 OVQLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYNMHWKQRPQGLEWIGEDIPSESNTNY 60
Db 20 OVQLOQPGAEVFKPGASVKLSCKASGYFTSYLHMVWQRPQGLEWIGRDPNNGGGTTY 79

QY 61 NQKFKGKATLTVDISSTAYMQLSLSLTSSEDSAVYVCARGYDGDWDYADYWGQGTSTV 117
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLSLTSSEDSAVYVCARYRLGRV-----FDYWGQGTTL 133

QY 118 TVSS 121
Db 134 TVSS 137
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RESULT 5
HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J00493: AAA38128.1; -.
DR PIR: A02028: HVM5G7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
```

```
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 71.3%; Score 469; DB 1; Length 140;
Best Local Similarity 73.6%; Pred. No. 3.6e-40;
Matches 89; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 OVQLOQPGAEVLKPGTSVKLSCKGKGYGTYFTSYNMHWKQRPQGLEWIGEDIPSESNTNY 60
Db 20 EVQLOQSGAEVLVRAGSSVKMSCKASGYFTSYGINVWQRPQGLEWIGYINPGNGYIN 79

QY 61 NQKFKGKATLTVDISSTAYMQLSLSLTSSEDSAVYVCARGYDGDWDYADYWGQGTSTV 120
Db 80 NEKFKGKATLTVDKSSSTAYMQLSLSLTSSEDSAVYFCARSHYGGSYDFDWGQGTPLTVS 139

QY 121 S 121
Db 140 S 140
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RESULT 6
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotypic response of the strain A mouse."
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR: A02028: HVM5G7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04EA4167B654AF CRC64;
```

```
Query Match 71.1%; Score 468; DB 1; Length 120;
Best Local Similarity 74.2%; Pred. No. 3.8e-40;
Matches 89; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 2 VOLQOPGAEVLKPGTSVKLSCKGKGYGTYFTSYNMHWKQRPQGLEWIGEDIPSESNTNY 61
Db 1 VOLQOPGAEVLVRAGSSVKMSCKASGYFTSYGINVWQRPQGLEWIGYINPGNGYKYN 60

QY 62 QKFKGKATLTVDISSTAYMQLSLSLTSSEDSAVYVCARGYDGDWDYADYWGQGTSTV 121
Db 61 EKFKGKATLTVDKSSSTAYMQLSLSLTSSEDSAVYFCARSHYGGSYDFDWGQGTPLTVS 120

RESULT 7
HV06_MOUSE STANDARD; PRT; 117 AA.
ID HV06_MOUSE
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
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Sat Apr 14 08:10:30 2001

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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR InterPro: IPR003006;
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 70.5%; Score 464; DB 1; Length 117;
Best Local Similarity 90.6%; Pred. No. 9.2e-40;
Matches 87; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 VOLOQPGAEVLKPGTSVKLSCKGYGTYFTSYWVHWKQPGGLEWIGETDPSNTN 61
DB 21 VOLOQPGAEVLKPGTSVKLSCKGYGTYFTSYWVHWKQPGGLEWIGETDPSNTN 80
QY 62 QKFKGKATLVDTSSSTAYMQLSLTSDSAVYYCA 97
DB 81 QKFKGKATLVDTSSSTAYMQLSLTSDSAVYYCA 116

RESULT 8
HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR InterPro: IPR003006;
DR Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 68.7%; Score 452; DB 1; Length 117;
Best Local Similarity 85.7%; Pred. No. 1.4e-38;
Matches 84; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYWVHWKQPGGLEWIGETDPSNTN 60
DB 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYWVHWKQPGGLEWIGETDPSNTN 79
QY 61 NQKFKGKATLVDTSSSTAYMQLSLTSDSAVYYCAR 98
DB 80 NQKFKGKATLVDTSSSTAYMQLSLTSDSAVYYCAR 117

RESULT 9
HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC EMBL; J00536; AAA38605.1;
CC PIR; A02031; HVM53.
CC InterPro: IPR003006;
CC Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;
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Query Match      68.5%; Score 451; DB 1; Length 117;
Best Local Similarity 87.8%; Pred. No. 1.8e-38;
Matches 86; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPTSVKLSCKGSGYFTSYMMHWKQRPQGGLEWIGEDIPDSNTNY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQPGAEIVKPTSVKLSCKASGYFTSYMDVWVQRPQGGLEWIGNIPDSSETHY 79
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSDSAVYICAR 98
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYICAR 117
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MMS4E.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match      67.9%; Score 447; DB 1; Length 117;
Best Local Similarity 71.1%; Pred. No. 4.6e-38;
Matches 86; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 1 QVQLQPGAEIVKPTSVKLSCKGSGYFTSYMMHWKQRPQGGLEWIGEDIPDSNTNY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLQSGPELVKPGASVKMSCKASGYFTDYMKWKQSHGKSLGWIGDINPNGGTSY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSDSAVYICARGYDGDWDYDVGQGTSTVS 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYICAR----DYDWDYDVGAGCTTTVS 116
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 S 121
Db 117 S 117

RESULT 11
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVM511.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match      67.9%; Score 447; DB 1; Length 121;
Best Local Similarity 69.4%; Pred. No. 4.8e-38;
Matches 84; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPTSVKLSCKGSGYFTSYMMHWKQRPQGGLEWIGEDIPDSNTNY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EAQLQSGAEIVKPTSVKLSCKAAGYFTNYWIGWKRPQGHGKLEWIGDIYPGGGFTNY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSDSAVYICARGYDGDWDYDVGQGTSTVS 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NDNLKGRKATLTADSSSTAYVQLSSLTSDSAIVHCARGIYNSPPYDWSGQGTTLTVS 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 S 121
Db 121 S 121

RESULT 12
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVM523.
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.

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AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 205..12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=84182519; PubMed=6201362;
RT Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RA "A V region determinant (idiotope) expressed at high frequency in B
RL lymphocytes is encoded by a large set of antibody structural genes.";
RT EMBO J. 3:517-523(1984).
RN PIR: A02040; MHMS38.
DR InterPro: IPR003006;
KW Fram; PF00047; -ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT FT DOMAIN 99 104
FT FT DOMAIN 105 118
FT FT DISULFID 22 96
FT FT NON_TER 118 118
FT FT SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
SQ
Query Match 67.1%; Score 441.5; DB 1; Length 118;
Best Local Similarity 70.5%; Pred. No. 1.6e-37;
Matches 86; Conservative 11; Mismatches 20; Indels 5; Gaps 2;
Qy 1 QVQLQQGAEALVRPGTSVKLSCKGYGTFTSYNMHWKQPPGGGLWICEIDPSESNTNY 60
Db :||||| :||||| :||||| :||||| :||||| :||| :||| :||| :|||
Qy 1 EVQLQQSGPELVKPGASVKISCKASGYTFDYNNMVKQSHGKSLEWIGDINPNNGTSY 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 NQKFGRATLTVDISSTAYMWOLSSLTSEDSAVVYCARG-GYGDWDYAIDYNQGQTSVT 119
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 120 SS 121
Db ||
Qy 117 SS 118
Db ||
RESULT 15
HV49_MOUSE STANDARD; PRG; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT rearranged VH gene segments.";
RL Cell 40:271-281(1985).
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DR EMBL: M13788; AAA38506.1; -.
DR PIR: A02035; MHMSB4.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match      67.0%; Score 441; DB 1; Length 117;
Best Local Similarity 84.5%; Pred. No. 1.8e-37;
Matches 82; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 2 VOLQPGAEVLVPGTSVKLSCKGYGTYTTSYWMHWVKRPGGLEWIGEIDPSESNTNYN 61
Db 21 VOLQPGAEVLVPGASVKLSCKASGYTTSYWMHWVKRPGGLEWIGNIDPNSGGTKYN 80
Qy 62 QKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCAR 98
Db 81 EKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYYCTR 117

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Search completed: April 13, 2001, 15:40:18
Job time: 271 sec

Result No.	Score	Query			DB	ID	Description
		Match	Length	Length			
1	473	71.9	117	11	Q9XE9	Q9XE9 mus musculus	
2	464.5	70.6	110	11	Q9JL77	Q9JL77 mus musculus	
3	462.5	70.3	114	11	Q9JL81	Q9JL81 mus musculus	
4	459	69.8	117	11	Q9XF0	Q9XF0 mus musculus	
5	458.5	69.7	118	11	Q9Z1C4	Q9Z1C4 mus musculus	
6	442.5	67.2	109	11	Q9JL75	Q9JL75 mus musculus	
7	437	66.4	117	11	Q9Z1C6	Q9Z1C6 mus musculus	
8	414.5	63.0	124	4	Q9UL92	Q9UL92 homo sapien	
9	414	62.9	119	4	Q9UL94	Q9UL94 homo sapien	
10	412.5	62.7	110	11	Q9JL83	Q9JL83 mus musculus	
11	390	59.3	123	4	Q9UL95	Q9UL95 homo sapien	
12	386	58.7	109	11	Q9JL85	Q9JL85 mus musculus	
13	356.5	54.2	116	4	Q9UL89	Q9UL89 homo sapien	
14	353.5	53.7	298	11	Q9QYF0	Q9QYF0 mus musculus	
15	352	53.5	150	4	Q9Y298	Q9Y298 homo sapien	
16	349	53.0	157	4	Q9Y578	Q9Y578 homo sapien	
17	323	49.1	116	4	Q9UL93	Q9UL93 homo sapien	
18	317	48.2	113	4	Q9UL90	Q9UL90 homo sapien	
19	313.5	47.6	147	4	Q9Y509	Q9Y509 homo sapien	

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Query Match      71.9%; Score 473; DB 11; Length 117;
Best Local Similarity 75.2%; pred. No. 4.2e-42;
Matches 91; Conservative 10; Mismatches 16; Indels 4; Caps 1;
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Query Match	71.9%;	Score 473;	DB 11;	Length 117;
Best Local Similarity	75.2%;	Pred. No. 4.2e-42;		
Matches	91;	Conservative 10;	Mismatches 16;	Indels 4; Gaps
1 QVQLQQGAEELVPGTYSVKLSCKGCGYFTT	SYMMHWVKQRPQGQGLEWIGEDPSESNTNY	60		
:	:	:	:	:
1 EVQLQQSGPELVKPGASVKMSCKASGYFTT	YMKWKQSHGKSLIEWIGDINPNGGTSY	60		
61 NQPFKQKATLTVDISSTAYMOLSLTSEDS	SAVYVCARGGYDGDWDAIDYWGOGTSVVTYS	120		
:	:	:	:	:
61 NQPFKQKATLTVDSKSTAYMOLSLTSEDS	SAVYVCARDRY----	YMDYWGOGTSVVTYS	116	
:	:	:	:	:

RESULT

```

Q9JL77
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206029; AAF69327.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 70.6%; Score 464.5; DB 11; Length 110;
Best Local Similarity 79.3%; Pred. No. 3e-41;
Matches 88; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 11 LVKPGTSVKLSCKGYGTYFTSYMHVHKQPGGGLWIGIDPSESNTYNNOKFKGKATL 70
DB 3 LVKPGASVKLSCKASGYFTTSSMHVAKQPGGGLWIGIEIHPSNGHTNNEKFKGKATL 62
QY 71 TVDISSTAYMQLSSITSEDSAVYICARGYDGDWYDAIDYWGQGTSTVTS 121
DB 63 TVDTSSSTAYVDLSSITSEDSAVYICAR---QRRNAMYDYGQGTSTVTS 110

RESULT 3
Q9JL81
ID Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206025; AAF69323.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match 70.3%; Score 462.5; DB 11; Length 114;
Best Local Similarity 77.9%; Pred. No. 5e-41;
Matches 88; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 10 ELVKPGTSVKLSCKGYGTYFTSYMHVHKQPGGGLWIGIDPSESNTYNNOKFKGKAT 69
DB 2 QLVKPGASVKLSCKASGYFTTSSMHVHKQPGGGLWIGIDPSESNTYNNOKFKGKAT 61
QY 70 LTVDISSTAYMQLSSITSEDSAVYICARGYDGDWYDAIDYWGQGTSTVTS 121
DB 62 LTVDKSSSTAYMQLSSITSEDSAVYICARSNYIGSSLYYFYDYGQGTTLTVSS 114

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RESULT 4
Q9QXF0
ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 69.8%; Score 459; DB 11; Length 117;
Best Local Similarity 72.7%; Pred. No. 1.2e-40;
Matches 88; Conservative 11; Mismatches 18; Indels 4; Gaps 1;

QY 1 QVLOQPGALVKPGTSVKLSCKGYGTYFTSYMHVHKQPGGGLWIGIDPSESNTY 60
DB 1 EVLOQSGPLVKPGASVKMSCKASGYFTDYMKVWKQSHGSKLSLEWIGDINPNGGTSY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSITSEDSAVYICARGYDGDWYDAIDYWGQGTSTVTS 120
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSITSEDSAVYICARDK---DYFDYWGQGTTLTVS 116
QY 121 S 121
DB 117 S 117

RESULT 5
Q9ZIC4
ID Q9ZIC4 PRELIMINARY; PRT; 118 AA.
AC Q9ZIC4
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matlis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT SEQUENCE 118 AA; 13035 MW; 90EEC559D31EC4FC CRC64;
SQ SEQUENCE 118 AA; 13035 MW; 90EEC559D31EC4FC CRC64;

Query Match 69.7%; Score 458.5; DB 11; Length 118;

```

Best Local Similarity 71.8%; Pred. No. 1.4e-40;
Matches 89; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
DB 1 QVQVQSGAELAPWASVKLSCKASGYFNSYMMQWVKQRPQGGLWIGAIYFGDGSY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCAR---GGYDGDWDYADYWGQGTSTV 117
DB 61 TQKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARRTVGGY-----FDYWGQGTTL 114
QY 118 TVSS 121
DB 115 TVSS 118

RESULT 6
Q9JL75
ID Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206031; AAF69329.1; -;
FT NON_TER 1
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 67.2%; Score 442.5; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 5.8e-39;
Matches 86; Conservative 8; Mismatches 14; Indels 5; Gaps 2;

QY 10 ELVKPGTSVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNYNKFQKAT 69
DB 1 ELVKPGASVAKMSCKASGYTFTSYMMHWVKQRPQGGLWIGIYINPDGTYNKFQKAT 60
QY 70 LTVDISSSTAYMQLSSLTSEDSAVYYCAR---GGYDGDWDYADYWGQGTSTVTVSS 121
DB 61 LTSDKSSSTAYMQLSSLTSEDSAVYYCARDGNRGP-----DYWGQGTTLTVSS 109

RESULT 7
Q9Z1C6
ID Q9Z1C6 PRELIMINARY; PRT; 117 AA.
AC Q9Z1C6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Watis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine

endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U78799; AAD00291.1; -;
DR INTERPRO: IPR003006; -;
DR PFAM: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193APB77E5B CRC64;

Query Match 66.4%; Score 437; DB 11; Length 117;
Best Local Similarity 70.2%; Pred. No. 2.4e-38;
Matches 85; Conservative 8; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
DB 1 QVQLQSGPOLVRPGTSVKLSCKASGYFTSYMMHWVKQRPQDLEWIGIDPSSEVKL 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGYDGDWDYADYWGQGTSTVTVS 120
DB 61 NQRLKDKAILTVDKSSNTAYMQFSGPTSEDSAVYYCTRGEV-SW---FAYWGQGTTLTVS 116
QY 121 S 121
DB 117 A 117

RESULT 8
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035022; AAD56258.1; -;
DR INTERPRO: IPR003006; -;
DR PFAM: PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 124
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAAACBD96ACD2A2 CRC64;

Query Match 63.0%; Score 414.5; DB 4; Length 124;
Best Local Similarity 64.5%; Pred. No. 5.7e-36;
Matches 80; Conservative 17; Mismatches 24; Indels 3; Gaps 1;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWVKQRPQGGLWIGIDPSESNTNY 60
DB 1 EVLVESGAELVKPGASVKLSCKASGYFTSSYYMMHWVKQRPQGGLWIGINFPSSGTSY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGYDGDWDYA---IDYWGQGTSTV 117
DB 61 AQKQGRVTMTDSTSTVYMEELSLRSEDSTAVYYCARGLYVVVPAAFSRFDYWGQGTTLV 120
QY 118 TVSS 121
DB 121 TVSS 124

RESULT 9

```
Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 62.9%; Score 414; DB 4; Length 119;
Best Local Similarity 65.6%; Pred. No. 6,le-36;
Matches 80; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 1 QVLOQPGAELVKPGTSVKLSCKGKGYFTSYMHVWVKRPGQGLEWIGEIDPSESNTNY 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
1 EVOLVESGAEVKPKGASVKVSKASGYFTGYMHVWVRAPQGLEWGWINPNSWTNY 60
QY 61 NQKFKGKATLTVDISSSTAYMOLSSLTSDSAVYCYARGYDG-WDYAIDYWGQTSVTV 119
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 AQKQGVGVTMTKDTSTAYMELSLRLSDDTAVYCYARGGGRLW---FDPWGQGLTVTV 117
QY 120 SS 121
Db ||
118 SS 119

RESULT 10
Q9JL83
ID Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69023.1; -
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 62.7%; Score 412.5; DB 11; Length 110;
Best Local Similarity 70.5%; Pred. No. 8e-36;
Matches 79; Conservative 8; Mismatches 22; Indels 3; Gaps 1;
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QY 10 ELVKPGTSVKLSCKGKGYFTSYMHVWVKRPGQGLEWIGEIDPSESNTNYNOKFKGKAT 69
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
2 ELVKPGASVKISCKASGYFTFSNMWVKLRPGQGLEWIGRIYPGDGYANGKFKGKAT 61
QY 70 LTVDISSTAYMOLSSLTSDSAVYCYARGYDGWDYDIDYWGQTSVTVSS 121
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
62 LTPADSSSTAYMOLSSLTSDSAVYFCAR---SNNDVRFAYWGQGLTVTVA 110

RESULT 11
Q9UL95
ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035019; AAD56255.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; Ig; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 59.3%; Score 390; DB 4; Length 125;
Best Local Similarity 60.0%; Pred. No. 2,le-33;
Matches 75; Conservative 16; Mismatches 30; Indels 4; Gaps 1;

QY 1 QVLOQPGAELVKPGTSVKLSCKGKGYFTSYMHVWVKRPGQGLEWIGEIDPSESNTNY 60
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
1 EVOLVESGAEVKPKGASVKVSKASGYFTGYMHVWVRAPQGLEWGWINPNSGTNY 60
QY 61 NQKFKGKATLTVDISSSTAYMOLSSLTSDSAVYCYAR---GGYDWDYDIDYWGQGS 116
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
61 AQKQGVGVTMTKDTSTAYMELSLRLSDDTAVYCYARGGGGRIAAAGDAFDWQGTM 120
QY 117 VTVSS 121
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
121 VTVSS 125

RESULT 12
Q9JL85
ID Q9JL85 PRELIMINARY; PRT; 109 AA.
AC Q9JL85;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
```


Db 20 QVQLVQSGAEVKKPGASVKVSCKVSGYTLITELPVHVGQAPGKGLEWVGSFDPESGESIY 79
Qy 61 NQKFKGKATLTVDISSSTAYMOLSLTSEDSAVYYCARGGYDGWDYAIDYWGQGTSTVTVS 120
Db 80 AREFOGSVMTADTSTDIAYMELSSLRSDDTAVYYCAVDPDPD- ---APDIWGQGTMTVTVS 135
Qy 121 S 121
Db 136 S 136

Search completed: April 13, 2001, 15:39:52
Job time: 264 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:33:41 ; Search time 57.59 seconds
(without alignments)
120.103 Million cell updates/sec

Title: US-08-700-737-9

Perfect score: 658

Sequence: 1 QVQLQPGAEIVRPGTSVKL.....DGWDYIDYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	140	19 W53815	Murine Act-1 heavy
2	658	100.0	144	19 W53816	Consensus protein
3	646	98.2	137	19 W53818	Protein sequence o
4	569	86.5	180	19 W53813	Heavy chain of a h
5	538	81.8	119	18 W07436	Anti-DNA antibody
6	536	81.5	119	16 R79863	Anti-EGFR antibody
7	523	79.5	464	19 W83041	Anti-Fas MAB HPE7A
8	523	79.5	464	21 B14747	Mouse anti-Fas ant
9	523	79.5	464	21 W90897	Murine anti-Fas an
10	520.5	79.1	122	16 R84555	B-cell lymphoma CH
11	520	79.0	119	16 R79861	Anti-EGFR antibody

12	520	79.0	445	16 R76085	MAB 55.1 heavy cha
13	520	79.0	464	16 R76088	MAB 55.1 heavy cha
14	518.5	78.8	118	18 W27122	Murine antibody he
15	517.5	78.6	269	15 R54756	PRAS111 between HI
16	517.5	78.6	269	15 R56482	ScFv PRAS107 and p
17	517.5	78.6	402	15 R56485	ScFv PRAS110 and p
18	517.5	78.6	435	15 R56483	ScFv PRAS108 and p
19	517	78.6	288	20 W82743	Fusion protein PNG
20	517	78.6	673	20 W82742	Plasmid PNG4/55.1s
21	516.5	78.5	120	15 R47493	Murine anti-CD18 A
22	513	78.0	119	18 W01578	Lead binding MAB 8
23	511	77.7	136	8 P70624	Sequence encoded b
24	511	77.7	136	18 W10584	Anti-hepatitis B h
25	511	77.7	136	18 W16340	Mouse-human chimae
26	511	77.7	136	18 W10239	Chimeric anti-hepa
27	511	77.7	136	19 W47510	Human anti-hepatit
28	511	77.7	136	19 W41054	Human anti-hepatit
29	511	77.7	136	19 W47517	Human anti-hepatit
30	511	77.7	136	20 W89535	Chimeric anti-hepa
31	510.5	77.6	256	13 R22568	ScFvB18 construct.
32	510.5	77.6	256	13 R22583	ScFvB18 construct
33	510.5	77.6	256	13 R22584	ScFvB18 construct
34	510.5	77.6	256	13 R22585	ScFvB18 construct
35	510.5	77.6	256	13 R22586	ScFvB18 construct
36	510.5	77.6	256	13 R22587	ScFvB18 construct
37	509.5	77.4	428	18 W24027	Single chain anti9
38	509.5	77.4	443	18 W24025	Single chain anti9
39	509.5	77.4	465	16 R66758	Anti-tobacco mosai
40	508	77.2	140	13 R27049	VH425 antibody clo
41	507	77.1	117	17 R88716	Mouse antibody hea
42	506.5	77.0	256	13 R22582	ScFvB18 construct
43	506.5	77.0	415	15 R56484	ScFv PRAS109 and p
44	505	76.7	119	21 Y92156	Murine 13B8 heavy
45	502.5	76.4	240	16 R85495	ScFv(FWP51). Synt

ALIGNMENTS

RESULT 1

W53815
ID W53815 standard; Protein; 140 AA.

XX AC W53815;

XX DT 14-JUL-1998 (first entry)

XX DE Murine Act-1 heavy chain variable region.

XX KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;

XX KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;

XX KW humanised antibody; murine antigen binding region; inhibition;

XX KW leukocyte infiltration of tissue; treatment; inflammatory disease;

XX KW inflammatory bowel disease.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT Peptide 1..19

XX FT Protein /note= "signal peptide"

XX FT Protein 20..140

XX FT Protein /note= "mature protein"

XX PN W09806248-A2.

XX PD 19-FEB-1998.

XX PF 06-AUG-1997; 97WO-US13884.

XX PR 15-AUG-1996; 96US-0700737.

XX PA (LEUK-) LEUKOSITE INC.

XX

Db 20 qvqlqpaaelvkpdtsvklscggygtyftsymhvwkqrpqgglewigeidpsesntny 79
 QY 61 NQKFKGKATLTVDISSRAYMOLSLTSDSAVYVCARGGYDGYDAIDYWGQGTSVTVS 120
 Db 80 nqkfgkatltvdisstaysmqlsltsedsavyyccarggydgydaidywgqgtsvtvs 139
 QY 121 S 121
 Db 140 s 140

RESULT 3
 W53818
 ID W53818 standard; Protein: 137 AA.

AC W53818;
 XX
 XX 14-JUL-1998 (first entry)
 DE Protein sequence of murine variable heavy chain region of clone H2B#34.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 XX
 OS Mus sp.
 OS WO9806248-A2.
 XX
 PN 19-FEB-1998.
 XX
 PD 06-AUG-1997; 97WO-US13884.
 XX
 PE 15-AUG-1996; 96US-0700737.
 XX
 PR (LEUK-) LEUKOSITE INC.
 XX
 PA Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX
 XX WPI; 1998-159172/14.
 DR N-PSDB; V20089.
 XX
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX
 XX Example 1; Fig 2; 145pp; English.

XX The present sequence represents the amino acid sequence comprising the
 CC variable region of murine Act-1 antibody determined from clone H2B#34.
 CC Act-1 is active against human alpha4-beta7 integrin. Muscosal adressin
 CC cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular
 CC integrin. The Act-1 antibody interferes with alpha4-beta7 integrin binding
 CC to MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. The present sequence was used to construct chimeric,
 CC humanised Act-1 antibodies, which contain murine antigen binding regions.
 CC The humanised immunoglobulin can be used to inhibit the interaction of
 CC cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7.
 CC It can be used for inhibiting leukocyte infiltration of tissues, e.g. for
 CC treating inflammatory diseases such as inflammatory bowel disease. The
 CC immunoglobulin can also be used for detection, isolation and diagnosis.
 XX Sequence 137 AA;

Query Match 98.2%; Score 646; DB 19; Length 137;
 Best Local Similarity 100.0%; Pred. No. 3-2e-46;
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQOPGAELVKPDTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSSENTNY 60

Db 20 qvqlqpaaelvkpdtsvklscggygtyftsymhvwkqrpqgglewigeidpsesntny 79
 QY 61 NQKFKGKATLTVDISSRAYMOLSLTSDSAVYVCARGGYDGYDAIDYWGQGTSVTVS 118
 Db 80 nqkfgkatltvdisstaysmqlsltsedsavyyccarggydgydaidywgqgtstvt 137

RESULT 4
 W53813
 ID W53813 standard; Protein: 180 AA.

AC W53813;
 XX
 XX 14-JUL-1998 (first entry)
 DE Heavy chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW humanised antibody; murine antigen binding region; inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20...180
 FT /note= "mature protein"

XX WO9806248-A2.
 XX
 PN 19-FEB-1998.
 XX
 PD 06-AUG-1997; 97WO-US13884.
 XX
 PE 15-AUG-1996; 96US-0700737.
 XX
 PR (LEUK-) LEUKOSITE INC.
 XX
 PA Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX
 XX WPI; 1998-159172/14.
 DR N-PSDB; V20076.

XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX
 XX Claim 20; Fig 11; 145pp; English.

XX The present sequence represents the heavy chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 XX Sequence 180 AA;

Query Match 86.5%; Score 569; DB 19; Length 180;
 Best Local Similarity 85.1%; Pred. No. 8.8e-40;

CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See T04011-T04026 and
 CC R79858-R79873)
 XX
 SQ Sequence 119 AA;

Query Match 81.5%; Score 536; DB 16; Length 119;
 Best Local Similarity 85.1%; Pred. No. 3e-37;
 Matches 103; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
 QY 1 QVQLQPGAEIVKPGTSVKLSCKGCGYGTFTSYMMHWVKQRPQGGLWIGELIDPSSTNTNY 60
 DB 1 EVQLQSGAEIVKPGTSVKLSCKGCGYGTFTSYMMHWVKQRPQGGLWIGELIDPSSTNTNY 60
 QY 61 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYGDWDYIDYWGQGTSTVTS 120
 DB 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYVCARGYGDWDYIDYWGQGTSTVTS 118
 QY 121 S 121
 DB 119 s 119

RESULT 7
 W83041 ID W83041 standard; Protein; 464 AA.
 AC W83041;
 DT 15-MAR-1999 (first entry)
 DE Anti-Fas MAB HFE7A heavy chain.
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region;
 CDR.

Mus musculus.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Sig_peptide 20..464
 FT Region /label= Mat_protein 20..140
 FT Region /label= Variable 141..464
 FT Region /label= Constant 50..54
 FT Region /label= CDR_H1 /note= "claim 9"
 FT Region /note= "claim 9"
 FT Region /label= CDR_H2 /note= "claim 9"
 FT Region /note= "claim 9"
 FT Region 118..128
 FT Region /label= CDR_H3 /note= "claim 9"
 XX AU9859701-A.
 XX

PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 PF
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S. Hideyuki H. Hiroko Y., Jun O., Kimihisa I;
 PI Masahiko O., Nobufusa S., Shin Y., Tohru T;
 XX
 DR WPI; 1998-543440/47.
 XX N-ESDB; V71029.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 FS Reference Example 4; Page 187-188; 292pp; English.
 XX

This is the amino acid of the heavy chain of murine anti-human Fas
 CC monoclonal antibody HFE7A. CNA (see V70129) encoding the heavy
 CC chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
 CC RNA by RT-PCR (see V70125-26). The invention provides humanised
 CC HFE7A antibodies (see W83031-37) produced by CDR grafting. These
 CC antibodies are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. They are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to treat
 CC such diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX

SQ Sequence 464 AA;

Query Match 79.5%; Score 523; DB 19; Length 464;
 Best Local Similarity 83.5%; Pred. No. 1.4e-35;
 Matches 101; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKGCGYGTFTSYMMHWVKQRPQGGLWIGELIDPSSTNTNY 60
 DB 20 QVQLQPGAEIVKPGTSVKLSCKGCGYGTFTSYMMHWVKQRPQGGLWIGELIDPSSTNTNY 79
 QY 61 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYVCARGYGDWDYIDYWGQGTSTVTS 120
 DB 80 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYVCARGYGDWDYIDYWGQGTSTVTS 139
 QY 121 S 121
 DB 140 s 140

RESULT 8
 BL4747 ID BL4747 standard; Protein; 464 AA.
 XX
 AC BL4747;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Mouse anti-Fas antibody HFE7A heavy chain.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

KW murine; complementarity determining region; CDR; human Fas;
 KW Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; heavy chain.
 OS Mus musculus.
 XX JP2000169393-A.
 XX 20-JUN-2000.
 XX 30-SEP-1999; 99JP-0278301.
 XX 30-SEP-1998; 98JP-0276883.
 XX (SANY) SANKYO CO LTD.
 XX WPI: 2000-485645/43.
 XX N-PSDB; A72108.
 XX preventive or treating agent for the diseases caused by an abnormality
 XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 XX anti-Fas antibody
 XX Example 4; Page 67-68; 139pp; Japanese.
 XX The invention relates to compositions for the prevention or treatment
 XX of diseases caused by an abnormality in the Fas/Fas ligand system
 XX containing an anti-Fas antibody as the active component. The anti-Fas
 XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 XX or a humanised version of HFE7A containing identical CDRs
 XX (complementarity determining regions) to antibody HFE7A. Via its
 XX interaction with Fas, the antibody of the invention acts as a modulator
 XX of apoptosis. The compositions of the invention may therefore be used in
 XX the treatment or prevention of conditions such as autoimmune diseases,
 XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 XX and organ graft rejection. The present sequence represents the
 XX heavy chain of the murine anti-human Fas monoclonal antibody HFE7A,
 XX which is produced by hybridoma HFE7A (FERM-AP-5828).
 XX Sequence 464 AA;
 SQ
 Query Match 79.5%; Score 523; DB 21; Length 464;
 Best Local Similarity 83.5%; Pred. No. 1.4e-35;
 Matches 101; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
 QY 1 QVQLQPGAEIVKPGTSTSVKLSCKGKGYTFTSYMMHWKQRPQGGLEWIGIDPSESTNTY 60
 DB 20 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYMMQWKQRPGGGLEWIGIDPDSYNTY 79
 QY 61 NQKPKKATLTVDISSTAYMQLSLITSEDSAVYCYARGYDWDYADYWGOGTSTVTS 120
 DB 80 NQKFKGKATLTVDSSTAYMQLSITSEDSAVYCYARNRDYNNWYFDWGTGTVTS 139
 QY 121 s 121
 DB 140 s 140
 RESULT 9
 W90897
 ID W90897 standard; Protein; 464 AA.
 XX AC W90897;
 XX 08-AUG-2000 (first entry)
 XX •Murine anti-Fas antibody HFE7A heavy chain protein.
 XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW

KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antirheosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;
 KW multiple sclerosis; Basedow's disease; arteriosclerosis; myocarditis;
 KW insulin dependent diabetes mellitus; glomerulonephritis; hepatitis; transplant rejection.
 XX Mus musculus.
 OS EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 XX 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 XX N-PSDB; A11546.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems
 XX Example reference 4; Page 100-102; 263pp; English.
 XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX ligand system, by binding to Fas on the cell surface, and prevents
 XX apoptosis in cells with a normal system, by inhibiting binding between
 XX Fas and its ligand. The products of the invention have anti-inflammatory,
 XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 XX immunomodulatory, dermatologic, immunosuppressive, thyromimetic,
 XX antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 XX antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 XX apoptosis by binding to cell surface Fas or inhibit it by competitive
 XX inhibition of ligand binding. (I) are used to treat and/or prevent
 XX diseases associated with the Fas/Fas ligand system, especially systemic
 XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 XX multiple sclerosis, Basedow's disease, arteriosclerosis, myocarditis,
 XX dependent diabetes mellitus, allergy, thrombopenia purpura, insulin
 XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 XX inhibit apoptosis in normal cells but selectively induce it in abnormal
 XX cells. They bind to both human and murine Fas, so can be evaluated in
 XX murine disease models. (I) act on the active site of Fas, i.e. they mimic
 XX the native ligand, do not induce liver disease, and have reduced risk of
 XX inducing a human anti-murine antibody response. This sequence represents
 XX a murine anti-Fas monoclonal antibody HFE7A heavy chain described in the
 XX method of the invention.
 XX Sequence 464 AA;
 SQ
 Query Match 79.5%; Score 523; DB 21; Length 464;
 Best Local Similarity 83.5%; Pred. No. 1.4e-35;
 Matches 101; Conservative 4; Mismatches 16; Indels 0; Gaps 0;
 QY 1 QVQLQPGAEIVKPGTSTSVKLSCKGKGYTFTSYMMHWKQRPQGGLEWIGIDPSESTNTY 60
 DB 20 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYMMQWKQRPGGGLEWIGIDPDSYNTY 79

QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYYCARGYDGDYDAIDYWGQGSTVTVS 120
 Db 80 ndkfgkcatltvdtssstaymqlssltssdsavyyccarnrdysnnwyfdwgtgttvtvs 139
 QY 121 S 121
 Db 140 S 140

RESULT 10

R84555
 ID R84555 standard; Protein; 122 AA.

XX AC R84555;

DT 02-FEB-1996 (first entry)

DE B-cell lymphoma CH12 IgM heavy chain.

KW Monoclonal antibody; Mab; SCH94.03; hybridoma; central nervous system;
 KW CNS; demyelination; multiple sclerosis; neural disease; therapeutic;
 KW B-cell lymphoma; CH12; IgM.

XX OS Mus sp.

XX PN W09530004-A1.

XX PD 09-NOV-1995.

XX PF 27-APR-1995; 95WO-US05262.

XX PR 29-APR-1994; 94US-0236520.

XX PA (MAYO-) MAYO FOUNDATION.

XX PI Miller DJ, Rodriguez M;

XX DR WPI; 1995-393077/50.

XX DR N-PSDB; T05314.

XX Monoclonal antibodies which stimulate central nervous system
 PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
 PT treating multiple sclerosis, and viral or post-neural diseases of
 PT the CNS.

XX PS Disclosure; Page 40; 63pp; English.

XX The heavy chain variable region amino acid sequence (given
 CC in R84554) of monoclonal antibody SCH94.03 shows extensive sequence
 CC similarity with the corresp. sequence (R84555) of the IgM produced
 CC by B-cell lymphoma CH12.

XX SQ Sequence 122 AA;

Query Match

Best Local Similarity 79.1%; Score 520.5; DB 16; Length 122;

Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLQQPQAEELVKPCTSVKLSCKGYGTYFTSYMMHWKQRPQGGLEWICEIDPSESNTNY 60

Db 1 qvqlqppgtelvkpgasvklscasgytftsywmhvwkqrpqgglewignpnsnggtny 60

QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYYCARGGY-DGDYDAIDYWGQGSTVTV 119

Db 61 nekfskatltvdkssstaymqlssltssdsavyyrydyrgsswgyyfdywggttlitv 120

QY 120 SS 121

Db 121 SS 122

RESULT 12

R76085

ID R76085 standard; Peptide; 445 AA.

XX

RESULT 11

R79861

ID R79861 standard; Protein; 119 AA.

XX AC R79861;

DT 02-JUL-1996 (first entry)

DE Anti-EGFR antibody heavy chain variable region (Clone L2 12B).

KW Single chain antibody; antibody; epidermal growth factor receptor;
 KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;
 KW assessment; phage antibody library.

XX OS Mus musculus.

XX PN W09525167-A1.

XX PD 21-SEP-1995.

XX PF 16-MAR-1995; 95WO-EP00978.

XX PR 02-DEC-1994; 94EP-0118970.

XX PR 17-MAR-1994; 94EP-0104160.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D;

PI Kettleborough AC, Mitjans F, Pluats J, Rosell E;

XX DR WPI; 1995-336972/43.

XX DR N-PSDB; T04014.

PT Anti-EGFR antibodies and single chain Fv antibody fragments -
 PT obtained from phage-antibody libraries, useful for diagnosis and
 PT therapy of tumours

XX PS Claim 4; Page 50; 93pp; English.

XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies
 CC and antibodies constructed from anti-EGFR antibody fragments can be
 CC used for diagnosis of tumours and assessment of tumour growth in
 CC vitro and in vivo. They may also be used in a pharmaceutical
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.
 CC The antibodies and fragments are derived from mice but are humanised
 CC so as to cause minimum reaction against them. They are produced
 CC using the phage antibody library. (See T04011-T04026 and
 CC R79858-R79873)

XX SQ Sequence 119 AA;

Query Match

Best Local Similarity 79.0%; Score 520; DB 16; Length 119;

Matches 99; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQQPQAEELVKPCTSVKLSCKGYGTYFTSYMMHWKQRPQGGLEWICEIDPSESNTNY 60

Db 1 qvqlqsgpeivkpgaalvklscasgytftsywmhvwkqrpqgglewigeidpsdystny 60

QY 61 NOKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYYCARGGYDGDYDAIDYWGQGSTVTVS 120

Db 61 nqkfgkatltvdkssstaymqlssltssdsavyyccarsdygsshf--dywgggtctvtvs 118

QY 121 S 121

Db 119 S 119

AC R76085;
 XX 21-NOV-1995 (first entry)
 DT XX
 XX DE MAB 55.1 heavy chain.
 XX
 XX
 XX Antigen binding structure; complementarity determining region; CDR;
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
 KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.
 XX
 XX Mus sp.
 XX
 PN WO9515382-A.
 XX
 XX 08-JUN-1995.
 PD
 XX
 XX 29-NOV-1994; 94WO-GB02610.
 PF
 XX
 PR 03-JUN-1994; 94GB-0011089.
 PR 03-DEC-1993; 93GB-0024819.
 XX
 XX (ZENE) ZENECA LTD.
 PA
 XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
 PI Rose MS, Wright AF;
 PI
 XX WPI; 1995-215262/28.
 DR
 XX Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 PT
 XX Claim 3; Page 97-98; 121pp; English.
 PS
 XX An antigen binding structure is based on the CDRs (given in R76078-
 CC 84) of the heavy (R76085) and light (R76086) chains of MAB 55.1
 CC (ECACC 93081901), which recognises the colorectal tumor-associated
 CC antigen CA55.1. It is optionally humanized and in the form F(ab')₂,
 CC F(ab)', Fab, Fv, scFv or V-min, and is produced in transgenic
 CC animals or plants.
 XX
 XX Sequence 445 AA;
 SQ

Query Match 79.0%; Score 520; DB 16; Length 445;
 Best Local Similarity 80.2%; Pred. No. 2.3e-35;
 Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKRGYGYFTFSYWMHWYKQRPQGQLEWIGEDIPSESNTNY 60
 |||||
 Db 1 qvqlqpgaeivkpgasvqlsckasgyftfgywlhwkqrpqgglewignpstgrsdy 60
 |||||

QY 61 NQPFKQATITVDISSSTAYMQLSLTSEDSAVYYCARGYDGDWDYDAIDYWGQGTSTVTS 120
 |||||
 Db 61 nekfkntatitvdksssttaysmqlssltseedsavyyccaraygyddamdywgqgtsvts 120
 |||||

QY 121 S 121
 Db 121 S 121

RESULT 13
 R76088
 ID R76088 standard; Protein; 464 AA.
 AC R76088;
 XX
 XX 21-NOV-1995 (first entry)
 DT XX
 XX MAB 55.1 heavy chain.
 DE XX

KW Antigen binding structure; complementarity determining region; CDR;
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
 KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.
 XX
 XX Mus sp.
 XX
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /label= sig_peptide
 FT Protein 20..464
 FT /label= Mat_protein
 FT /note= "claim 3, page 97-98"
 XX
 XX
 PN WO9515382-A.
 XX
 XX 08-JUN-1995.
 PD
 XX
 XX 29-NOV-1994; 94WO-GB02610.
 PF
 XX
 PR 03-JUN-1994; 94GB-0011089.
 PR 03-DEC-1993; 93GB-0024819.
 XX
 XX (ZENE) ZENECA LTD.
 PA
 XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
 PI Rose MS, Wright AF;
 PI
 XX WPI; 1995-215262/28.
 DR N-PSDB; Q94037.
 DR
 XX Antigen binding structures containing CDRs recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the
 PT diagnosis and therapy of cancer
 PT
 XX Disclosure; Fig.15; 121pp; English.
 PS
 XX MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036)
 CC chains of 55.1 were isolated, and F(ab)', F(ab')₂, Fab, Fv, scFv or
 CC V-min humanized 55.1 constructs have been expressed in myeloma
 CC cells and E. coli.
 XX
 XX Sequence 464 AA;
 SQ

Query Match 79.0%; Score 520; DB 16; Length 464;
 Best Local Similarity 80.2%; Pred. No. 2.4e-35;
 Matches 97; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKRGYGYFTFSYWMHWYKQRPQGQLEWIGEDIPSESNTNY 60
 |||||
 Db 20 qvqlqpgaeivkpgasvqlsckasgyftfgywlhwkqrpqgglewignpstgrsdy 79
 |||||

QY 61 NQPFKQATITVDISSSTAYMQLSLTSEDSAVYYCARGYDGDWDYDAIDYWGQGTSTVTS 120
 |||||
 Db 80 nekfkntatitvdksssttaysmqlssltseedsavyyccaraygyddamdywgqgtsvts 139
 |||||

QY 121 S 121
 Db 140 S 140

RESULT 14
 W27122
 ID W27122 standard; Protein; 118 AA.
 XX
 XX W27122;
 AC
 XX 04-JAN-1998 (first entry)
 DT XX
 XX Murine antibody heavy chain variable region consensus.
 DE

XX Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
 KW human milk fat globule; HMF; tumour; breast cancer; vaccine.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers
 XX 31..35
 FT Region /label= CDR1
 FT /note= "complementarity determining region 1"
 FT 50..66
 FT Region /label= CDR2
 FT /note= "complementarity determining region 2"
 FT 99..107
 FT Region /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Misc-difference 100
 FT /note= "unspecified amino acid residue"
 FT Misc-difference 101
 FT /note= "unspecified amino acid residue"
 FT Misc-difference 102
 FT /note= "unspecified amino acid residue"

WO9722699-A2.

26-JUN-1997.

19-DEC-1996; 96WO-US20757.

13-DEC-1996; 96US-0575762.

20-DEC-1995; 95US-0575762.

26-JAN-1996; 96US-0591965.

(KENT) UNIV KENTUCKY.

Chatterjee M, Chatterjee SK, Foon KA;

WPI; 1997-341690/31.

Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
 against human milk fat globule disease associated tumours,
 especially breast cancer

Example 2; Fig 26C; 130pp; English.

This polypeptide sequence comprises a consensus sequence of murine
 heavy chain variable regions (VH) selected on the basis of identity
 to the VH region (see W27120) of monoclonal anti-idiotypic antibody
 11D10. The sequences were obtained from a GenBank database
 search. A VL consensus (W27121) was also produced. 11D10 has at
 least 18 departures from the consensus sequences (7 in the light
 chain and 11 in the heavy chain). 8 occur within CDRs and 10
 outside CDRs. 11D10 polypeptides and polynucleotides can be
 used in vaccines and pharmaceutical compositions for the treatment
 of human milk fat globule-associated diseases such as breast
 cancer.

Sequence 118 AA;

Query Match 78.8%; Score 518.5; DB 18; Length 118;
 Best Local Similarity 81.8%; Pred. No. 8e-36;
 Matches 99; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLQPGAEIVKPGTYSVKLSCKGYGTYFTSYWHVHWKQPPGQGLEWIGEDPSNTNY 60
 DB 1 qvqlqsgaelvrpgasvmsckasyfttsyvmhwkvrpggglwlaipyngdntny 60
 QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYVCARGYDCWDVAIDWVGOGTSVTVS 120
 DB 61 nqkfkgtatltdststaymqllssltseedsavvfcarxxxg---amdywgggtsvtvs 117
 QY 121 S 121

Db 118 s 118

RESULT 15

R54756
 ID R54756 standard; Protein; 269 AA.

XX AC R54756;

XX DT 06-DEC-1994 (first entry)

XX DE PRAS111 between HindIII and EcoRI sites.

XX Single chain Fv fragment; ScFv; Gene Therapy; Adenovirus;
 KW Penton fibre; Ad5; Fusion sites; PCR; polymerase chain reaction.
 XX OS Synthetic.

XX Key Location/Qualifiers
 FT Protein 1..269
 FT /label= Single chain Fv fragment
 FT Peptide 1..22
 FT /label= pelB leader peptide
 FT Protein 23..142
 FT /label= heavy chain variable region
 FT Region 23..51
 FT /label= VH FR1
 FT Region 52..57
 FT /label= VH CDR 1
 FT Region 58..71
 FT /label= VH FR2
 FT Region 72..86
 FT /label= VH CDR 2
 FT Region 89..120
 FT /label= VH FR3
 FT Region 121..131
 FT /label= VH CDR 3
 FT Region 132..142
 FT /label= VH FR4
 FT Peptide 143..265
 FT /label= (G4S)3 Linker
 FT Protein 158..269
 FT /label= Light chain variable region
 FT Region 158..179
 FT /label= VL FR1
 FT Region 180..193
 FT /label= VL CDR 1
 FT Region 194..207
 FT /label= VL FR2
 FT Region 208..215
 FT /label= VL CDR 2
 FT Region 216..247
 FT /label= VL FR3
 FT Region 248..256
 FT /label= VL CDR 3
 FT Region 257..269
 FT /label= VL FR3

WO9410323-A.

11-MAY-1994.

04-NOV-1993; 93WO-CB02267.

04-NOV-1992; 92GB-0023084.

(IMCR) IMPERIAL CANCER RES TECHNOLOGY.

Epenetos AA, Spooner RA;

WPI; 1994-167477/20.
 N-PSDB; Q64817.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2001, 17:35:04 ; Search time 4.45 seconds
(without alignments)
47.200 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQPGAEIVKPTSVKL.....DGWDYADYWGQTSVTSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7695 seqs, 1735856 residues

Total number of hits satisfying chosen parameters: 7695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	73.9	140	4	US-08-475-815A-11
2	426	64.7	132	5	US-09-386-658-2
3	278.5	42.3	482	5	US-09-509-031-16
4	242	36.8	240	5	US-09-782-504-4
5	107	16.3	155	5	US-09-509-031-11
6	107	16.3	342	5	US-09-509-031-6
7	107	16.3	495	5	US-09-509-031-7
8	105	16.0	128	4	US-08-475-815A-7
9	69.5	10.6	442	5	US-09-739-449-9534
10	65.5	10.0	914	5	US-09-193-562D-28
11	65	9.9	753	1	PCT-US01-09226-51
12	64	9.7	281	5	US-09-739-449-11638
13	62.5	9.5	109	5	US-09-386-658-4
14	62.5	9.5	170	5	US-09-814-950-4
15	62.5	9.5	172	5	US-09-814-950-2
16	62	9.4	517	5	US-09-739-449-12328
17	60.5	9.2	1008	5	US-09-308-453-2
18	60	9.1	757	5	US-09-739-449-11939
19	59.5	9.0	639	5	US-09-739-449-11223
20	59	9.0	574	5	US-09-815-108-7
21	58.5	8.9	342	5	US-09-815-108-20
22	58.5	8.9	379	5	US-09-813-408-6
23	58.5	8.9	448	5	US-09-815-108-6
24	58.5	8.9	472	5	US-09-815-108-5
25	58.5	8.9	504	5	US-09-815-108-8
26	58.5	8.9	504	5	US-09-815-108-15
27	58.5	8.9	504	5	US-09-815-108-17

28	58.5	8.9	504	5	US-09-815-108-19
29	58.5	8.9	509	5	US-09-815-108-3
30	58.5	8.9	529	5	US-09-815-108-2
31	58.5	8.9	594	5	US-09-815-108-22
32	57	8.7	251	5	US-09-739-449-12898
33	56	8.5	652	5	US-09-813-742-5
34	56	8.5	1144	5	US-09-813-742-3
35	55.5	8.4	571	5	US-09-809-391-481
36	55	8.4	101	5	US-09-809-391-754
37	55	8.4	215	5	US-09-739-449-10936
38	55	8.4	216	5	US-09-739-449-12644
39	55	8.4	238	5	US-09-809-391-485
40	54.5	8.3	178	5	US-09-509-031-13
41	54.5	8.3	198	5	US-09-509-031-8
42	54.5	8.3	358	5	US-09-739-449-11717
43	54	8.2	299	5	US-09-739-449-9917
44	54	8.2	1758	5	US-09-739-449-11627
45	53.5	8.1	249	5	US-09-739-449-8182

ALIGNMENTS

RESULT 1
US-08-475-815A-11
; Sequence 11, Application US/08475815A
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIO LABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; TITLE OF INVENTION: LYMPHOMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-815A-11

Sequence 19, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 12898, A
Sequence 5, Appl
Sequence 3, Appl
Sequence 481, App
Sequence 754, App
Sequence 10936, A
Sequence 12644, A
Sequence 485, App
Sequence 13, Appl
Sequence 11717, A
Sequence 9917, Ap
Sequence 11627, A
Sequence 8182, Ap


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Query Match          16.0%; Score 105; DB 4; Length 128;
Best Local Similarity 27.0%; Pred. No. 3e-05; Gaps 7;
Matches 33; Conservative 23; Mismatches 46; Indels 20; Gaps 7;

QY      1 QVQLQQPGAEFL-VKPGTSYKLSCKGYGYFTSYWMHWKORPGGLE-WIGEIDPSESNT 58
Db      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      23 QIVLSQSPAILASPGEKYMTICRA---SSVSYSIHWFQKPGSPKPMI--YATSNLAS 77
Db      23 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      59 NYNQKFKGKATLVDITSSSTAY-MQLSLLTSEDSANYYCARGYDGDWDAIDYWGOGTSV 117
Db      59 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      78 GVPVRFSGS-----GSGTYSLTISRVEADAATYYCQQ-----WTSNPPTFGGGTKL 125
Db      78 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      118 TV 119
Db      126 EI 127

RESULT          9
US-09-739-449-9534
; Sequence 9534, Application US/09739449
; GENERAL INFORMATION: Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9534

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 753
; TYPE: PR1
; ORGANISM: Homo sapiens
PCT-US01-09226-51

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[illegible]

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RESULT 12
US-09-739-449-11638
: Sequence 11638, Application US/09739449
: GENERAL INFORMATION:
: APPLICANT: Hinkle, Gregory J.
: TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(13490)C
: CURRENT APPLICATION NUMBER: US/09/739,449
: CURRENT FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: US 09/514,000
: PRIOR FILING DATE: 2000-02-23
: NUMBER OF SEQ ID NOS: 13351
: SEQ ID NO 11638
: LENGTH: 281
: TYPE: PRT
: ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11638

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Query Match      9.7%: Score 64; DB 5; Length 281;
Best Local Similarity 25.8%; pred. No. 1.3;
Matches 23; Conservative 17; Mismatches 35; Indels 14; Gaps 4;

QY      24  GYCYTTSTVMHWVKORPCQGLEIGEDIPDESNTNTNQRFKGKATLTVDISSTAYMOL 83
      | | | | : | | | | | : | | : | | : | | : | | : | | : | | :
Db      90  GVGYQENYF-----RSDVTLDYMGKSRDFRGSTGFCGSGVPGR-C-VSADLSLSLAYTILM 142

QY      84  SS-----LTSEDSAVYYCA---RGYDGDWD 105
      : : | | | | | | | | | | | | | | | | | | | | | |
Db     143  ANAYVDLGLTYGSIPTPYGVGGIGGSGVVKWD 171

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RESULT 13
US-09-386-658-4
; Sequence 4, Application US/09386658
; GENERAL INFORMATION:
; APPLICANT: Erlanger, Bernard
; APPLICANT: Chen, Bi-Xing
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575-54182/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/386,658
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-09-386-658-4

```

ORGANISM: mouse
US-09-386-658-4

[illegible]

```

RESULT      14
US-09-814-950-4
; Sequence 4, Application US/09814950
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Human
US-09-814-950-4

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Query Match          9.5%; Score 62.5; DB 5; Length 170;
Best Local Similarity 21.3%; pred. No. 1;
Matches 20; Conservative 9; Mismatches 36; Indels 29; Gaps 1;

Qy      3 QLOQGAELVPGTSTVKLSCRGYGTFTSYWMHWKRPQGOGLEWIGIDPSESNTNYNQ 62
       | : | : | | : : | : | | | |
Db      62 QISOPEVYAAPGESLEVRCLLDKAAVISMTKDGVLHGPNNRTVLCE----- 109

Qy      63 KFKKGATLTVIDSSAYMQLSSLTSEDSAVYYC 96
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Db     110 -----YLQIKGATPRDGLGYAC 126
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RESULT      15
US-09-814-950-2
; Sequence 2, Application US/09814950
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human
US-09-814-950-2

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Query Match 9.5%; Score 62.5; DB 5; Length 172;
Best Local Similarity 21.3%; Pred. No. 1;
Matches 20; Conservative 9; Mismatches 36; Indels 29; Gaps 1;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:35:03 ; Search time 117.03 Seconds
(without alignments)
166.311 Million cell updates/sec

Title: US-08-700-737-9

Perfect score: 658

Sequence: 1 QVQLQPGAEELVKPGTSVKL.....DGWDYADYWGQGTSTVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
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- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
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- 19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US060_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	121	11 US-08-700-737-9	Sequence 9, Appl
2	658	100.0	140	11 US-08-700-737-15	Sequence 15, Appl
3	658	100.0	144	11 US-08-700-737-2	Sequence 2, Appl
4	646	98.2	137	11 US-08-700-737-4	Sequence 4, Appl
5	572	86.9	121	11 US-08-700-737-55	Sequence 55, Appl
6	572	86.9	180	11 US-08-700-737-19	Sequence 19, Appl
7	536	81.5	119	9 US-08-073-967-44	Sequence 44, Appl
8	536	81.5	119	9 US-08-553-497-12	Sequence 12, Appl
9	525	79.8	127	11 US-08-700-737-53	Sequence 53, Appl
10	524	79.6	119	8 US-08-443-540-62	Sequence 62, Appl

11	523	79.5	464	14	US-09-053-583-9	Sequence 9, Appl
12	523	79.5	464	18	US-09-408-646-9	Sequence 9, Appl
13	523	79.5	464	18	US-09-499-662-9	Sequence 9, Appl
14	520.5	79.1	122	10	US-08-892-084-28	Sequence 28, Appl
15	520.5	79.1	122	11	US-08-779-784-28	Sequence 28, Appl
16	520.5	79.1	122	17	US-09-322-862-28	Sequence 28, Appl
17	520	79.0	119	9	US-08-553-497-8	Sequence 8, Appl
18	518.5	78.8	118	11	US-08-766-350-48	Sequence 48, Appl
19	518.5	78.8	118	11	US-08-766-350A-48	Sequence 48, Appl
20	518.5	78.8	118	12	US-08-836-455-48	Sequence 48, Appl
21	517.5	78.6	269	15	US-09-120-809-72	Sequence 72, Appl
22	517.5	78.6	269	17	US-09-313-928-3	Sequence 3, Appl
23	517.5	78.6	402	17	US-09-313-928-9	Sequence 9, Appl
24	517.5	78.6	415	17	US-09-313-928-7	Sequence 7, Appl
25	517.5	78.6	435	17	US-09-313-928-5	Sequence 5, Appl
26	517	78.6	119	8	US-08-443-540-61	Sequence 61, Appl
27	516.5	78.5	120	4	US-08-024-712-6	Sequence 6, Appl
28	516	78.4	119	8	US-08-443-540-63	Sequence 63, Appl
29	513.5	78.0	120	3	US-07-881-109-21	Sequence 21, Appl
30	513.5	78.0	120	3	US-07-881-109A-21	Sequence 21, Appl
31	513.5	78.0	120	7	US-08-313-198-21	Sequence 21, Appl
32	513.5	78.0	120	11	US-08-720-323-21	Sequence 21, Appl
33	513	78.0	119	8	US-08-443-540-60	Sequence 60, Appl
34	513	78.0	119	8	US-08-462-798-6	Sequence 6, Appl
35	513	78.0	119	9	US-08-541-373-6	Sequence 6, Appl
36	513	78.0	119	9	US-08-541-373A-6	Sequence 6, Appl
37	508	77.2	140	8	US-08-487-165-24	Sequence 24, Appl
38	507	77.1	117	15	US-09-157-370-2	Sequence 2, Appl
39	505	76.7	119	18	US-09-406-532-2	Sequence 2, Appl
40	502.5	76.4	240	15	US-09-159-027-4	Sequence 4, Appl
41	502.5	76.4	241	3	US-07-828-832-11	Sequence 11, Appl
42	502.5	76.4	241	8	US-08-465-473A-11	Sequence 11, Appl
43	502.5	76.4	637	3	US-07-828-832-16	Sequence 16, Appl
44	502.5	76.4	637	8	US-08-465-473A-16	Sequence 16, Appl
45	501	76.1	111	8	US-08-443-540-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-700-737-9
Sequence 9, Application US/08700737
GENERAL INFORMATION:
APPLICANT: Ponath, Paul D.
APPLICANT: Ringler, Douglas J.
APPLICANT: Jones, S. Tarran
APPLICANT: Newman, Walter
APPLICANT: Saldanha, Jos
APPLICANT: Bendig, Mary M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
TITLE OF INVENTION: INTEGRIN
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,737
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS95-10

us-08-700-737-9.rapm

Sat Apr 14 08:10:28 2001

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-700-737-9

Query Match      100.0%; Score 658; DB 11; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
Db 1 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
Db 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
QY 121 S 121
Db 121 S 121

RESULT 2
US-08-700-737-15
; Sequence 15, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-15
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Query Match      100.0%; Score 658; DB 11; Length 140;
Best Local Similarity 100.0%; Pred. No. 8.6e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
Db 20 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
Db 80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 139
QY 121 S 121
Db 140 S 140

RESULT 3
US-08-700-737-2
; Sequence 2, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-2

Query Match      100.0%; Score 658; DB 11; Length 144;
Best Local Similarity 100.0%; Pred. No. 8.8e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 60
Db 20 QVQLQPGAEIVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGGLEWIGEDIDPSESNTNY 79
QY 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 120
Db 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 139
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```

RESULT 7
US-08-073-967-44
; Sequence 44, Application US/08073967
; GENERAL INFORMATION:
; APPLICANT: Syamal K. Datta
; TITLE OF INVENTION: METHODS FOR INHIBITING THE
; TITLE OF INVENTION: ACTIVITY OF PATHOGENIC T
; TITLE OF INVENTION: HELPER CELLS ASSOCIATED WITH
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,967
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/764,686
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
;

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Query Match	81.5%;	Score 536;	DB 9;	Length 119;
Best Local Similarity	85.1%;	Pred. No. 9,7e-46;		
Matches 103; Conservative	4;	Mismatches 12;	Indels	2; Gaps
QY	1	QVQLQQPGAEIVKPTSVKLCKGCGYTFTSYMMHWVKRPPQGLEGWIGEIDPSSSNTNY	60	
		: : : : : : : : : :		
Dd	1	EVLQOOGSAELVKPGASVXLCKASKGYTFTSYMMHWVKRPPQGLEGWIGEIDPSSDNTNY	60	
		: : : : : : : : : :		
Qy	61	NQRFKGKATLTVDISSTAYMQLSSLTSDESAVYYCARGYGDWDAIDYWGGGTSTVTVS	120	
		: : : : : : : : : :		
Dd	61	NQRFKGKATLTVDKSSSTAYMQLSSLTSDESAVYYCARSDYGSSHFF--DYWGQGTTVTYS	118	
Qy	121	s	121	s
Dd	119	s	119	s

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; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-21107.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 CIOOTTI UD
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-443-540-62

Query Match 79.6%; Score 524; DB 8; Length 119;
Best Local Similarity 83.7%; Pred. No. 1.5e-44;
Matches 103; Conservative 5; Mismatches 9; Indels 6; Gaps

QY 1 QVQLQQGAEVLVPGTTSVKLSCKGYTFTSYMMHWVKORPGGLEWIGEDPSDSNTNY 60
Db 1 QVQLLESAGAEVLVPGASVKLSCKASGYTFTSYMMHWVKORPGGLEWIGEDPSDSYTY 60
QY 61 NQRFKGRKATLVDISSTAYMQLSSLTSEDSAVYYCARG--GYDGDWDYAIYWGQGTSTV 118
Db 61 NQRFKGRKATLVDKSSSTAYMQLSSLTSEDSAVYYCAKGLRLY----FAMDYWGQGTSTV 118
QY 119 VSS 121
Db 117 VSS 119

RESULT 11
US-09-053-583-9
; Sequence 9, Application US/09053583A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Ohtsumi, Jun
; APPLICANT: Ohtsumi, Masahiko
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Yoshida, Hiroko
; APPLICANT: Shiraishi, Akio
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126/HG
; CURRENT APPLICATION NUMBER: US/09/053,583A
; CURRENT FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: JP HEI 9-82953
; EARLIER FILING DATE: 1997-04-01
; EARLIER APPLICATION NUMBER: JP HEI 9-169088
; EARLIER FILING DATE: 1997-06-25
; EARLIER APPLICATION NUMBER: JP HEI 9-276064
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.0

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US-08-692-084-28

Query Match 79.1%; Score 520.5; DB 10; Length 122;
Best Local Similarity 81.1%; Pred. No. 3.5e-44;
Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

Qy 1 QVQLQQPGAEVLKPGTSVKLSCKGCGYGTFTSYNMHWKQRPQGLEWIGEDIPSESNTNY 60
Db 1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYNMHWKQRPQGLEWIGNINPSNGGTNY 60
Qy 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGY-DGWDYDAIDYWGQGTSTVTV 119
Db 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYIYARDYGYSSWGYFDYWGQGTTLTV 120
Qy 120 SS 121
Db 121 SS 122

RESULT 15

US-08-779-784-28
; Sequence 28, Application US/08779784
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-784-28

Query Match 79.1%; Score 520.5; DB 11; Length 122;
Best Local Similarity 81.1%; Pred. No. 3.5e-44;
Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

Qy 1 QVQLQQPGAEVLKPGTSVKLSCKGCGYGTFTSYNMHWKQRPQGLEWIGEDIPSESNTNY 60
Db 1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYNMHWKQRPQGLEWIGNINPSNGGTNY 60
Qy 61 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGGY-DGWDYDAIDYWGQGTSTVTV 119
Db 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYIYARDYGYSSWGYFDYWGQGTTLTV 120
Qy 120 SS 121
Db 121 SS 122

Search completed: April 13, 2001, 17:37:47
Job time: 164 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:34:02 ; Search time 28.17 Seconds
(without alignments)
82.517 Million cell updates/sec

Title: US-08-700-737-9
Perfect score: 658
Sequence: 1 QVQLQQPGLVLPCTSVKL.....DGWDYADYWGQTSVTVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	536	81.5	119	2	US-08-553-497A-12
2	524	79.6	119	3	US-08-881-037-62
3	520.5	79.1	122	1	US-08-236-520-9
4	520.5	79.1	122	5	PCT-US95-05262-9
5	520	79.0	119	2	US-08-553-497A-8
6	520	79.0	445	1	US-08-353-400-33
7	520	79.0	464	1	US-08-353-400-36
8	517.5	78.6	269	2	US-08-428-257A-72
9	517.5	78.6	269	2	US-08-491-988-3
10	517.5	78.6	402	2	US-08-491-988-9
11	517.5	78.6	415	2	US-08-491-988-7
12	517.5	78.6	435	2	US-08-491-988-5
13	517	78.6	119	3	US-08-881-037-61
14	516	78.4	119	3	US-08-881-037-63
15	513	78.0	119	3	US-08-881-037-60
16	513	78.0	119	3	US-08-881-037-60
17	508	77.2	140	1	US-07-946-421-24
18	502.5	76.4	241	1	US-08-235-838-11
19	502.5	76.4	241	1	US-08-235-838-11
20	502.5	76.4	637	1	US-08-465-473B-11
21	502.5	76.4	637	2	US-08-465-473B-16
22	501	76.1	111	3	US-08-881-037-14
23	500	76.0	244	2	US-08-553-497A-20
24	500	76.0	246	2	US-08-553-497A-24
25	498	75.7	116	2	US-08-737-560A-7
26	496	75.4	143	1	US-08-236-520-7
27	496	75.4	143	5	PCT-US95-05262-7

28 495 75.2 139 2 US-08-894-922A-5
29 495 75.2 252 2 US-08-894-922A-14
30 495 75.2 271 2 US-08-894-922A-10
31 494 75.1 111 3 US-08-881-037-16
32 494 75.1 118 3 US-09-065-059-5
33 494 75.1 119 2 US-08-737-560A-10
34 494 75.1 136 5 PCT-US93-11611-4
35 494 75.1 244 2 US-08-553-497A-22
36 493.5 75.0 120 1 US-08-211-202-1
37 493.5 75.0 246 1 US-08-469-486-57
38 493.5 75.0 246 2 US-08-469-658-57
39 493 74.9 111 3 US-08-881-037-17
40 493 74.9 242 2 US-08-553-497A-26
41 490 74.5 111 3 US-08-881-037-15
42 489 74.3 138 1 US-08-482-882-78
43 489 74.3 138 2 US-08-483-389-78
44 489 74.3 138 2 US-08-487-113D-78
45 489 74.3 138 3 US-08-714-017-78

ALIGNMENTS

RESULT 1
US-08-553-497A-12
; Sequence 12, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLERBROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAM, JAUME
; APPLICANT: MITJANS, FRANCES
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 12:

Sequence 5, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 16, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 4, Appl
Sequence 22, Appl
Sequence 1, Appl
Sequence 57, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 26, Appl
Sequence 15, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 78, Appl

us-08-700-737-9.ra1

Sat Apr 14 08:10:28 2001

2;

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-12

Query Match 81.5%; Score 536; DB 2; Length 119;

Best Local Similarity 85.1%; Pred. No. 3.4e-42;

Matches 103; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKORPGGLEWIGEDIDPSESNTNY 60
DB 1 EVQLQSGAEVLKPGASVKLSCKASGYTFTSYMMHWKORPGGLEWIGEDIDPDSYNTY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGYDGYDAIDYWGQGTSTVTS 120
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYICARSDYSSHF--DYWGQGTITVTS 118

QY 121 S 121

DB 119 S 119

RESULT 2

US-08-881-037-62

; Sequence 62, Application US/08881037

; Patent No. 6080588

; GENERAL INFORMATION:

; APPLICANT: Glick, Gary D.

; APPLICANT: Swanson, Patrick C.

; TITLE OF INVENTION: DNA BINDING ANTIBODIES

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/881.037

; FILING DATE: 23-JUN-1997

; CLASSIFICATION: 530

; PRIOR APPLICATION NUMBER: US 08/443,540

; APPLICATION NUMBER: 530

; FILING DATE: 18-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kanski, Antoinette F.

; REGISTRATION NUMBER: 34,202

; REFERENCE/DOCKET NUMBER: 203442110710

; TELEPHONE: (650) 813-5600

; TELEFAX: (650) 494-0792

; TELEX:

; INFORMATION FOR SEQ ID NO: 62:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-881-037-62

Query Match 79.6%; Score 524; DB 3; Length 119;

Best Local Similarity 83.7%; Pred. No. 4.2e-41;

2;

Matches 103; Conservative 5; Mismatches 9; Indels 6; Gaps 1;
QY 1 QVQLQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKORPGGLEWIGEDIDPSESNTNY 60
DB 1 QVQLLESAGAEVLKPGASVKLSCKASGYTFTSYMMHWKORPGGLEWIGEDIDPDSYTY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARG--GYDGDYDAIDYWGQGTSTV 118
DB 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYICAKRLRY---FAMDYWGQGTSTV 116
QY 119 VSS 121
DB 117 VSS 119

RESULT 3

US-08-236-520-9

; Sequence 9, Application US/08236520

; Patent No. 5591629

; GENERAL INFORMATION:

; APPLICANT: Rodriguez, Moses

; APPLICANT: Miller, David J.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE

; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/236,520

; FILING DATE: 29-APR-1994

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 27,227

; REFERENCE/DOCKET NUMBER: MMV92-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 122 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-236-520-9

Query Match 79.1%; Score 520.5; DB 1; Length 122;

Best Local Similarity 81.1%; Pred. No. 9e-41;

Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKORPGGLEWIGEDIDPSESNTNY 60
DB 1 QVQLQPGTELVKPGASVKLSCKASGYTFTSYMMHWKORPGGLEWIGINISNGTNY 60
QY 61 NQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYICARGY--DGWDYDAIDYWGQGTSTV 119
DB 61 NEKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYIYARDYVYSSWGYFDYWGQGTTLV 120
QY 120 SS 121
DB 121 SS 122

RESULT 4
 PCT-US95-05262-9
 : Sequence 9, Application PC/TUS9505262
 : GENERAL INFORMATION:
 : APPLICANT: Mayo Foundation for Medical Education Research
 : TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
 : TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
 : STREET: Two Militia Drive
 : CITY: Lexington
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02173
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US95/05262
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: U.S. 08/236,520
 : FILING DATE: April 29, 1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Granahan, Patricia
 : REGISTRATION NUMBER: 27,227
 : REFERENCE/DOCKET NUMBER: MMV92-01 PCT
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-861-6240
 : TELEFAX: 617-861-9540
 : INFORMATION FOR SEQ ID NO: 9:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 122 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : PCT-US95-05262-9

Query Match 79.1%; Score 520.5; DB 5; Length 122;
 Best Local Similarity 81.1%; Pred. No. 9e-41;
 Matches 99; Conservative 4; Mismatches 18; Indels 1; Gaps 1;
 QY 1 QVLOQPQGAELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGQGLEWIGEDIPSESNTNY 60
 Db 1 QVLOQPQGTLYKPGASVKLSCKASGYTFTSYMMHWVKORPGQGLEWIGINPNSGGTNY 60
 QY 61 NQKFKGKATLVDISSTAYMQLSSLTSEDSAVYYCARGGY-DGWDYDAIDYWGQGTSTVTV 119
 Db 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYARDYDYGSSNGYFYDWGGQTTLTV 120
 QY 120 SS 121
 Db 121 SS 122

RESULT 5
 US-08-553-497A-8
 : Sequence 8, Application US/08553497A
 : Patent No. 5844093
 : GENERAL INFORMATION:
 : APPLICANT: KETTLEBOROUGH, C. A.
 : APPLICANT: BENDIG, MARY M.
 : APPLICANT: ANSELL, KEITH H.
 : APPLICANT: GUSOW, DETLEF
 : APPLICANT: ADAM, JAUME
 : APPLICANT: MITJANS, FRANCESCA
 : APPLICANT: ROSELL, ELISABET

: APPLICANT: BLASCO, FRANCESCA
 : APPLICANT: PIULATS, JAUME
 : TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 : TITLE OF INVENTION: ANTIBODIES
 : NUMBER OF SEQUENCES: 30
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 : STREET: 2200 CLARENDON BLVD. SUITE 1400
 : CITY: ARLINGTON
 : STATE: VA
 : COUNTRY: US
 : ZIP: 22201
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/553.497A
 : FILING DATE: 17-NOV-1995
 : CLASSIFICATION: 530
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: WO PCT/EP95/00978
 : FILING DATE: 16-MAR-1995
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 94104160.0
 : FILING DATE: 17-MAR-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 94118970.6
 : FILING DATE: 02-DEC-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: HAMLET-KING, DIANA
 : REGISTRATION NUMBER: 33,302
 : REFERENCE/DOCKET NUMBER: MERCK 1726
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 703-243-6333
 : TELEFAX: 703-243-6410
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 119 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-553-497A-8

Query Match 79.0%; Score 520; DB 2; Length 119;
 Best Local Similarity 81.8%; Pred. No. 9.8e-41;
 Matches 99; Conservative 6; Mismatches 14; Indels 2; Gaps 1;
 QY 1 QVLOQPQGAELVKPGTSVKLSCKGKGYTFTSYMMHWVKORPGQGLEWIGEDIPSESNTNY 60
 Db 1 QVLOQESGPELVKPGALVKLSCKASGYTFTSYMMHWVKORPGQGLEWIGEDIPSDSYTN 60
 QY 61 NQKFKGKATLVDISSTAYMQLSSLTSEDSAVYYCARGGYDGMVDYDAIDYWGQGTSTVTV 120
 Db 61 NQKFKGKATLTVDKSSNTAYMQLSSLTSEDSAVYYCARGDYGSSHP--DWGGQTTTVTS 118
 QY 121 S 121
 Db 119 S 119

RESULT 6
 US-08-353-400-33
 : Sequence 33, Application US/08353400
 : Patent No. 5665357
 : GENERAL INFORMATION:
 : APPLICANT:
 : TITLE OF INVENTION: PROTEINS
 : NUMBER OF SEQUENCES: 37
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-988-7

Query Match 78.6%; Score 517.5; DB 2; Length 415;
Best Local Similarity 81.8%; Pred. No. 6.7e-40;
Matches 99; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVLOQPAGELVKPGTSVKLSCKGCGYGTFTSYMMHWKQRPQGLEWIGEDIPSESNTNY 60

Db 23 QVLOQPAGELVKPGASVKLSCKASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGGTKY 82

QY 61 NOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGYDGDYDAIDYWGQGTSTVTS 120

Db 83 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYGGSSY-FDYWGQGTSTVTS 141

QY 121 S 121

Db 142 S 142

RESULT 12

US-08-491-988-5

; Sequence 5, Application US/08491988

; Patent No. 5973116

; GENERAL INFORMATION:

; APPLICANT: EPENETOS, AGAMENNON A.

; APPLICANT: SPOONER, ROBERT A.

; APPLICANT: LEONARAIN, MAHENDRA

; TITLE OF INVENTION: Compounds for targeting

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP

; STREET: 261 MADISON AVENUE

; CITY: NEW YORK

; STATE: NY

; COUNTRY: USA

; ZIP: 10016-2391

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/491,988

; FILING DATE: 18-DEC-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: GOLDBERG, JULES E.

; REGISTRATION NUMBER: 24,408

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-986-4090

; TELEFAX: 212-818-9479

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 435 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-491-988-5

Query Match 78.6%; Score 517.5; DB 2; Length 435;
Best Local Similarity 81.8%; Pred. No. 7.1e-40;
Matches 99; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVLOQPAGELVKPGTSVKLSCKGCGYGTFTSYMMHWKQRPQGLEWIGEDIPSESNTNY 60

Db 23 QVLOQPAGELVKPGASVKLSCKASGYTFTSYMMHWKQRPGRGLEWIGRIDPNSGGTKY 82

QY 61 NOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARGYDGDYDAIDYWGQGTSTVTS 120

Db 83 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYGGSSY-FDYWGQGTSTVTS 141

QY 121 S 121

Db 142 S 142

RESULT 13

US-08-881-037-61

; Sequence 61, Application US/08881037

; Patent No. 6080588

; GENERAL INFORMATION:

; APPLICANT: Swanson, Patrick C.

; TITLE OF INVENTION: DNA BINDING ANTIBODIES

; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/881,037

; FILING DATE: 23-JUN-1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/443,540

; FILING DATE: 18-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Kanski, Antoinette F.

; REGISTRATION NUMBER: 34,202

; REFERENCE/DOCKET NUMBER: 203442110710

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 813-5600

; TELEFAX: (650) 494-0792

; TELEX:

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-881-037-61

Query Match 78.6%; Score 517; DB 3; Length 119;

Best Local Similarity 82.1%; Pred. No. 1.18e-40;

Matches 101; Conservative 6; Mismatches 10; Indels 6; Gaps 2;

QY 1 QVLOQPAGELVKPGTSVKLSCKGCGYGTFTSYMMHWKQRPQGLEWIGEDIPSESNTNY 60

Db 1 QVQLLESGVELVKPGASVKLSCKASGYTFTSYMMHWKQRPQGLEWIGEDIPSDSYTY 60

QY 61 NOKFKGKATLTVDISSTAYMQLSSLTSEDSAVYYCARG--GYDGDYDAIDYWGQGTSTV 118

Db 61 NOKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAKRLRY---FAMDYWGQGTSTV 116

QY 119 VSS 121

Db 117 VSS 119

RESULT 14

US-08-881-037-63

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:36:46 ; Search time 32.39 Seconds
(without alignments)
280.069 Million cell updates/sec

Title: US-08-700-737-12
Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPYTFGGGKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues
Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	620	89.2	132	B25912	Ig kappa chain pre
2	576	82.9	113	H30560	Ig kappa chain v r
3	574	82.6	113	E30560	Ig kappa chain v r
4	563	81.0	112	S37203	Ig kappa chain v r
5	560.5	80.6	131	B39276	Ig kappa chain pre
6	553.5	79.6	131	B34904	Ig kappa chain pre
7	549.5	79.1	131	C34904	Ig kappa chain pre
8	548.5	78.9	114	PL0202	Ig kappa chain pre
9	546.5	78.6	131	B32513	anti-DNA autoantib
10	546.5	78.6	131	B30577	Ig kappa chain pre
11	545.5	78.5	131	D34904	Ig kappa chain pre
12	540.5	77.8	132	PH0106	Ig kappa chain pre
13	539	77.6	131	D29380	anti-digoxin trans
14	537.5	77.3	111	PS0074	Ig kappa chain pre
15	537.5	77.3	131	G34903	Ig kappa chain v r
16	536.5	77.2	131	S09259	Ig kappa chain pre
17	529.5	76.2	131	S52449	Ig kappa chain pre
18	523.5	75.3	131	PT0178	Ig kappa chain v r
19	521	75.0	130	C29380	Ig kappa chain pre
20	502	72.2	133	S23230	Ig kappa chain pre
21	497.5	71.6	119	A49032	Ig kappa chain v r
22	496	71.4	142	S22502	Ig kappa chain v r
23	493.5	71.0	118	S24503	Ig kappa chain v r
24	493	70.9	133	S42611	HUNYK protein prec
25	492.5	70.9	118	S24536	Ig kappa chain v r
26	491	70.6	133	K24HURP	Ig kappa chain pre
27	490.5	70.6	118	S24533	Ig kappa chain v r
28	489	70.4	112	E27887	Ig kappa chain v r
29	488.5	70.3	118	S24500	Ig kappa chain v r

```

30      488      70.2      112      2      A31807      Ig kappa chain v r
31      488      70.2      118      2      PT0359      Ig kappa chain v r
32      487.5      70.1      118      2      S24529      Ig kappa chain v r
33      487.5      70.1      118      2      S24535      Ig kappa chain v r
34      486      69.9      112      2      A49713      Ig kappa chain v r
35      486      69.9      219      2      S16112      Ig kappa chain v r
36      484      69.6      110      2      S26335      Ig kappa chain v r
37      484      69.6      121      2      S67944      Ig kappa chain v r
38      483      69.5      112      2      S32189      Ig kappa chain BrE
39      483      69.5      113      2      PL0203      Ig kappa chain v r
40      481.5      69.3      118      2      S24552      anti-DNA autoantib
41      481.5      69.3      140      2      S22658      Ig kappa chain v r
42      481      69.2      112      2      B31485      Ig kappa chain pre
43      481      69.2      219      2      FC4203      Ig kappa chain v r
44      480.5      69.1      118      2      S24530      Ig kappa chain v r
45      480      69.1      112      2      D27887      Ig kappa chain v r

```

ALIGNMENTS

```

RESULT 1
B25912
Ig kappa chain precursor V region (W3129) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C:Accession: B25912
R:Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A:Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light
A:Reference number: A94147; MUID:87175689
A:Accession: B25912
A:Molecule type: mRNA
A:Residues: 1-132 <BOR>
A:Cross-references: GB:M15874; NID:g196839; PIDN:AAA38796.1; PID:g196840
A:Note: the authors translated the codon CTC for residue 120 as Ser
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence (fragment) #status predicted <SIG>
F:20-132/Product: Ig kappa chain v region W3129 #status predicted <VAR>
F:35-114/Domain: immunoglobulin homology <IMM>

```

```

Query Match      89.2%; Score 620; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 2.3e-47;
Matches 118; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 3 LPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDVSTSCRSSQSLAKYGNWYLSWYL 62
    ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 LPVRLVLLFWIPASRGVVVVTQTPLSLPVSGDVSTSCRSSQSLATSHGTYLSWYL 61

QY 63 HKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTFTLKIKPEDLGMVYCLQGTHPVY 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 HKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTFTLKIKPEDLGMVYCLQGTHPVY 121

QY 123 FGGGKLEIK 132
    ||| ||||| ||
Db 122 FGAGTKLEIK 131

```

```

RESULT 2
H30560
Ig kappa chain v region (36.1.2D) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: H30560
R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono
A:Reference number: A30560; MUID:89110062
A:Accession: H30560
A>Status: preliminary

```

Sat Apr 14 08:10:19 2001

A:Molecule type: mRNA
A:Residues: 1-113 <MAT>
A:Cross-references: GB:M24275; NID:g197085; PIDN:AAA63372.1; PID:g197086
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 576; DB 2; Length 113;
Best Local Similarity 97.3%; Pred. No. 1.3e-43;
Matches 109; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 21 DVVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 80
|||||
Db 1 DVVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 60
|||||

QY 81 SGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQPTFTGGGKLEIK 132
|||||
Db 61 SGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQPTFTGGGKLEIK 112
|||||

RESULT 3
E30560
Ig kappa chain V region (16.4.12E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 21-Jul-2000
C:Accession: E30560
R:Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibody 3A3
A:Reference number: A30560; MUID:89110062
A:Accession: E30560
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAT>
A:Cross-references: GB:M24272; NID:g197079; PIDN:AAA63369.1; PID:g197080
A:Note: the author's translated the codon GTA for residue 30 as His
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 574; DB 2; Length 113;
Best Local Similarity 97.3%; Pred. No. 2e-43;
Matches 109; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 DVVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 80
|||||
Db 1 DVVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 60
|||||

QY 81 SGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQPTFTGGGKLEIK 132
|||||
Db 61 SGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQPTFTGGGKLEIK 112
|||||

RESULT 4
S37203
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S37203
R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of TMV-specific monoclonal antibodies.
A:Reference number: S37200
A:Accession: S37203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <FTS>
A:Cross-references: EMBL:X74588; NID:g402597; PIDN:CAA52665.1; PID:g1333980
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 563; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.8e-42;
Matches 106; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DVVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 80
|||||
Db 1 DVVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGISNRF 60
|||||

QY 81 SGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQPTFTGGGKLEIK 132
|||||
Db 61 SGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQPTFTGGGKLEIK 112
|||||

RESULT 5
B39276
Ig light chain precursor V-D-J region (6-19) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: B39276
R:Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A:Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis
A:Reference number: A39276; MUID:91088540
A:Accession: B39276
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <REI>
A:Cross-references: GB:M55313; NID:g198095; PIDN:AAA63385.1; PID:g198096
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 80.6%; Score 560.5; DB 2; Length 131;
Best Local Similarity 80.3%; Pred. No. 3.5e-42;
Matches 106; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGGDDVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSW 60
|||||
Db 1 MKLPVRLVLLFWIPVSGGDDVVTQTLSLPVSGDQVSISSRSQSLAKSYGNTYLSW 59
|||||

QY 61 YLHKPGQSPQLLIYGISNRFSGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQ 120
|||||
Db 60 YLHKPGQSPQLLIYGISNRFSGVPRDFSGSGGTDFTLKISTIKPEDLGMYYCLOQTHQ 119
|||||

QY 121 YTFGGGKLEIK 132
|||||
Db 120 YTFGGGKLEIK 131
|||||

RESULT 6
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; B34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-
A:Reference number: A34903; MUID:90094387
A:Accession: B34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 553.5; DB 2; Length 131;

C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 546.5; DB 2; Length 131;
Best Local Similarity 79.5%; Pred. No. 5.9e-41;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQTPLSPVSLGDQASISCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGQ3POLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHOP 120
DB 60 YLQKPGQ3PKVLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
DB 120 FTFGGTLEIK 131

RESULT 11
D34904
Ig kappa chain precursor V region (3-13) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: D34904
R:Bedzyk, W.D.; Harron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 263, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive V region of mouse Ig kappa chain precursor V region
A:Reference number: A34903; MUID:90094387
A:Accession: D34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:Cross-reference: GB:L39105; NID:9639658; PIDN:AAA61590.1; PID:9639659
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 545.5; DB 2; Length 131;
Best Local Similarity 78.8%; Pred. No. 7.2e-41;
Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQTPLSPVSLGDQASISCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGQ3POLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHOP 120
DB 60 YLQKPGQ3PKVLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
DB 120 FTFGGTLEIK 131

RESULT 12
PH0106
anti-digoxin transfectoma antibody heavy chain V region precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
C:Accession: PH0106
R:Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
Mol. Immunol. 27, 901-909, 1990
A:Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
A:Reference number: PH0105; MUID:91015092
A:Accession: PH0106
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <NEA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 540.5; DB 2; Length 132;
Best Local Similarity 79.5%; Pred. No. 2e-40;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQTPLSPVSLGDQASISCRSSQSLVHSGNTYLSW 59
QY 61 YLHKPGQ3POLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHOP 120
DB 60 YLQKAGQ3PKVLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
QY 121 YTFGGGTLEIK 132
DB 120 FTFGGTLEIK 131

RESULT 13
D29380
Ig kappa chain precursor V region (B003 46/2D7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: D29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable region of mouse Ig kappa chain precursor V region
A:Reference number: A92612; MUID:88007582
A:Accession: D29380
A:Molecule type: mRNA
A:Residues: 1-131 <CHE>
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 539; DB 2; Length 131;
Best Local Similarity 78.8%; Pred. No. 2.6e-40;
Matches 104; Conservative 8; Mismatches 18; Indels 2; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQTPLSPVSLGDQASISCRSSQSLVHSGNTYLSW 58
QY 61 YLHKPGQ3POLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOQTHOP 120
DB 59 YLQKPGQ3PKVLIYKVSNNRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHLP 118
QY 121 YTFGGGTLEIK 132
DB 119 RTFGGTLEIK 130

RESULT 14
PS0074
Ig kappa chain V region (38C13.V7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0074
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement of the immunoglobulin V region
A:Reference number: A92781; MUID:89310348
A:Accession: PS0074
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-111 <LEV>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:40:18 ; Search time 21.32 Seconds
(without alignments)
212.088 Million cell updates/sec

Title: US-08-700-737-12
Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLQGTHTQPTFGGCKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	70.6	133	1 KV2F_HUMAN	P06310 homo sapien
2	471	67.8	113	1 KV2G_MOUSE	P01631 mus musculus
3	422	60.7	117	1 KV2E_HUMAN	P06309 homo sapien
4	418	60.1	113	1 KV2D_HUMAN	P01617 homo sapien
5	416.5	59.9	115	1 KV2A_HUMAN	P01614 homo sapien
6	410	59.0	113	1 KV2B_HUMAN	P01615 homo sapien
7	401	57.7	129	1 KV3L_HUMAN	P18135 homo sapien
8	400	57.6	129	1 KV3M_HUMAN	P18136 homo sapien
9	395.5	56.9	112	1 KV2C_HUMAN	P01616 homo sapien
10	395	56.8	112	1 KV2F_MOUSE	P01629 mus musculus
11	394	56.7	113	1 KV2D_MOUSE	P01630 mus musculus
12	392	56.4	113	1 KV2E_MOUSE	P03976 mus musculus
13	387.5	55.8	131	1 KV3I_MOUSE	P01661 mus musculus
14	385.5	55.4	134	1 KV4C_HUMAN	P06314 homo sapien
15	380.5	54.7	128	1 KV3K_HUMAN	P06311 homo sapien
16	378	54.4	133	1 KV4B_HUMAN	P01658 mus musculus
17	373.5	53.7	132	1 KV3F_MOUSE	P01627 mus musculus
18	372	53.5	120	1 KV2B_MOUSE	P01628 mus musculus
19	369	53.1	113	1 KV2C_HUMAN	P04207 homo sapien
20	368	52.9	129	1 KV3H_HUMAN	P01626 mus musculus
21	367	52.8	112	1 KV2A_MOUSE	P01634 mus musculus
22	366.5	52.7	136	1 KV5B_MOUSE	P01660 mus musculus
23	359.5	51.7	111	1 KV3H_MOUSE	P01664 mus musculus
24	356.5	51.3	111	1 KV3L_MOUSE	P04431 homo sapien
25	356.5	51.3	129	1 KV1W_HUMAN	P01625 homo sapien
26	354.5	51.0	114	1 KV4A_HUMAN	P04433 homo sapien
27	353.5	50.9	115	1 KV3I_HUMAN	P01662 mus musculus
28	352.5	50.7	108	1 KV1_CANFA	P01633 mus musculus
29	350.5	50.4	111	1 KV3_MOUSE	P01637 mus musculus
30	350.5	50.4	149	1 KV5A_MOUSE	P01665 mus musculus
31	347.5	50.0	128	1 KV5E_MOUSE	P04432 homo sapien
32	346.5	49.9	111	1 KV3M_MOUSE	
33	345.5	49.7	129	1 KV1X_HUMAN	

34	345	49.6	108	1 KV3A_HUMAN	P01619 homo sapien
35	345	49.6	109	1 KV3B_HUMAN	P01620 homo sapien
36	344.5	49.6	111	1 KV3A_MOUSE	P01654 mus musculus
37	344	49.5	116	1 KV3J_HUMAN	P04434 homo sapien
38	343.5	49.4	111	1 KV3O_MOUSE	P01667 mus musculus
39	341.5	49.1	108	1 KV1M_HUMAN	P01605 homo sapien
40	341.5	49.1	111	1 KV3D_MOUSE	P03977 mus musculus
41	340.5	49.0	111	1 KV3N_MOUSE	P01666 mus musculus
42	340	48.9	112	1 KV3B_MOUSE	P01655 mus musculus
43	339.5	48.8	111	1 KV3C_MOUSE	P01656 mus musculus
44	338.5	48.7	111	1 KV3Q_MOUSE	P01669 mus musculus
45	338.5	48.7	111	1 KV3R_MOUSE	P01670 mus musculus

ALIGNMENTS

RESULT 1

KV2F_HUMAN

ID KV2F_HUMAN STANDARD; PRT; 133 AA.

AC P06310;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041852; PubMed=2997711;

RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;

RT "Human immunoglobulin kappa light chain genes of subgroups II and

III."

RL Nucleic Acids Res. 13:6499-6513(1985).

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CC -----

DR EMBL; Z00020; CAA77315.1; -

DR PIR; A01890; K2HURP.

DR InterPro; IPR003006; -

DR Pfam; PF00047; Ig; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.

FT DOMAIN 21 43 FRAMEWORK 1.

FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 60 74 FRAMEWORK 2.

FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 82 113 FRAMEWORK 3.

FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 123 132 FRAMEWORK 4.

FT DISULFID 43 113 BY SIMILARITY.

FT NON_TER 133 133

SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match

Best Local Similarity 70.6%; Score 491; DB 1; Length 133;

Matches 91; Conservative 19; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLPVPSFGDVSIICRSQSLSKSYGNTYLSW 60

Db 1 MRUPAQLGLLMLVPGSGDVVMTQSPVLPVLPQSPASISCRSSQSLVSDGNTYLNW 60

QY 61 YLHKPQSPQLIYIGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMVYCYLQGTQHP 120

RX MEDLINE=84191506; PubMed=6325927;
 RA Klobbeck H.G., Solomon A., Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain
 RL diversity";
 CC Nature 309:73-76(1984).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z00009; NOT_ANNOTATED_CDS.
 DR PIR: A01889; K2HUGM.
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
 FT DOMAIN 27
 FT DOMAIN 28 43 FRAMEWORK 1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 59 65 FRAMEWORK 2.
 FT DOMAIN 66 97 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 98 106 FRAMEWORK 3.
 FT DOMAIN 107 116 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 27 97 FRAMEWORK 4.
 FT NON_TER 117 117 BY SIMILARITY.
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 60.7%; Score 422; DB 1; Length 117;
 Best Local Similarity 71.3%; Pred. No. 2.2e-35;
 Matches 82; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 QY 18 SGDDVVVTPSLPVSFGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPOLLYIGIS 77
 DB 2 SSGDIVMTQSPSLPVTGPAPASISCRSSQSLHSGNYLWYLOKPGQSPOLLYIGIS 61
 QY 78 NRESGVDPDRFSGSGGTDFTLKISTIKPEDLGMYYCLOGTHQPTFGGKLEIK 132
 DB 62 NRASGVDPDRFSGSGGTDFTLKISRVEAEDGVYVCMQGLQPTPTGQGTKEIK 116

RESULT 4
 ID KV2D_HUMAN STANDARD; PRT: 113 AA.
 AC P01617;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION TEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE=74148480; PubMed=4596149;
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
 RT "Amino acid sequence of a kappa Bence Jones protein from a case of
 RT primary amyloidosis";
 RL Biochemistry 12:3763-3780(1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE=73166638; PubMed=4700495;
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
 RA Glenner G.G.;
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a
 RT patient with plasma cell dyscrasia and amyloidosis.";

Db 61 FQORPCQ:PRRLIYKVSNRDSDVDFSGSGGTDFTLKISRVEAEDGVYVCMQGTWS 120
 QY 121 YTFGGTILEIK 132
 Db 121 WTFGGTIVEIK 132
 RESULT 2
 KV2G_MOUSE STANDARD; PRT: 113 AA.
 ID P01631;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION 26-10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=1090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=83173921; PubMed=6404298;
 RA Novotny J., Margolies M.N.;
 RT "Amino acid sequence of the light chain variable region from a mouse
 RT anti-digoxin hybridoma antibody";
 RL Biochemistry 22:1153-1158(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
 CC PROTEIN THAT BINDS DIGOXIN.
 DR PIR: A01914; KVMS26
 DR InterPro: IPR003006;
 DR Pfam: PF00047; Ig; 1.
 DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.
 KW DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 40 54 FRAMEWORK 2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 62 93 FRAMEWORK 3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 103 112 FRAMEWORK 4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 67.8%; Score 471; DB 1; Length 113;
 Best Local Similarity 80.4%; Pred. No. 2.9e-40;
 Matches 90; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
 QY 21 DVVVTQ:PLSLPVSFGDQVSISSRSQSLAKSYGNTYLSWYHLKPGQSPOLLYIGISNRF 80
 DB 1 DVVVTQ:PLSLPVSIGDQASISCRSSQSLHSGNYLWYLOKAGQSPKLLIYKVSNRF 60
 QY 81 SGVDPRI:SGSGSGGTDFTLKISTIKPEDLGMYYCLOGTHQPTFGGKLEIK 132
 DB 61 SGVDPRI:SGSGSGGTDFTLKISRVEAEDGLVFCSTHTVPTFGGKLEIK 112

RESULT 3
 ID KV2E_HUMAN STANDARD; PRT: 117 AA.
 AC P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RL J. Clin. Invest. 52:1276-1281(1973).
 CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
 CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
 CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
 CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1.2)
 CC MARKER.
 DR PIR; A01886; K2HUTW.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 60.1%; Score 418; DB 1; Length 113;
 Best Local Similarity 69.6%; Pred. No. 5.4e-35;
 Matches 78; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
 QY 21 DVVVTQPLSLPVSGDQVSIICRSQSLAKSYGNTYLSWYHLKPKQSPOLLIIYISNRF 80
 DB 1 DIVMTQSPSLPVTGEPASISCRSSQSLHSDGFDYLNWYLRKQKQSPZLLIYALSNA 60
 QY 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
 DB 61 SGVPDRFSGSGGTDFTLKISRVEADGVVYCMZALQAPITFGGKTRLEIK 112

RESULT 5
 KV2A_HUMAN
 ID KV2A_HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION CUM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=68242259; PubMed=5586923;
 RX Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
 type).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 96 AND 97.
 RX MEDLINE=70063440; PubMed=4181819;
 RA Hilschmann N.;
 RT "Molecular basis of antibody formation.";
 RL Naturwissenschaften 56:195-205(1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01885; K2HUCM.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 24 95
 FT NON_TER 115
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 59.9%; Score 416.5; DB 1; Length 115;

Best Local Similarity 72.6%; Pred. No. 7.8e-35;
 Matches 82; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
 QY 21 DVVVTQPLSLPVSGDQVSIICRSQSLAKS-YNTYLSWYHLKPKQSPOLLIIYISNRF 79
 DB 2 DIVMTQSPSLPVTGEPASISCRSSQSLDSDGNTYLNWYLRKQKQSPOLLIIYISNRF 61
 QY 80 FSGVPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
 DB 62 ASGVPDRFSGSGGTDFTLKISRVAEDGVVYCMQORLEIPTFGGKLEIR 114

RESULT 6
 KV2B_HUMAN
 ID KV2B_HUMAN STANDARD; PRT; 113 AA.
 AC P01615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION FR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76253627; PubMed=821524;
 RA Riesen W.F., Jaton J.-C.;
 RT "Variable region sequence of the light chain from a Waldenström's IgM
 RT with specificity for phosphorylcholine.";
 RL Biochemistry 15:3829-3833(1976).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
 DR PIR; A01886; K2HUF.
 DR InterPro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 39
 FT DOMAIN 40 54
 FT DOMAIN 55 61
 FT DOMAIN 62 93
 FT DOMAIN 94 102
 FT DOMAIN 103 112
 FT DISULFID 23 93
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 59.0%; Score 410; DB 1; Length 113;
 Best Local Similarity 68.8%; Pred. No. 3.4e-34;
 Matches 77; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 QY 21 DVVVTQPLSLPVSGDQVSIICRSQSLAKSYGNTYLSWYHLKPKQSPOLLIIYISNRF 80
 DB 1 DVVMTQSPFLPVTGEPASISCRSSQSLVYRGTLYLWYLRKQKQSPOLLIIYISNRF 60
 QY 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
 DB 61 SGVPDRFSGSGGTDFTLKISRVAEDGVVYCMQATZSPYTFGGGKLEIK 112

RESULT 7
 KV3L_HUMAN
 ID KV3L_HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

Sat Apr 14 08:10:20 2001

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO022; K3HUHA.
DR HSP: P01789; 2MCP.
DR InterPro: IPI003006; -.
DR Pfam: PF00047; ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 57.7%; Score 401; DB 1; Length 129;
Best Local Similarity 56.8%; Pred. No. 3.1e-33;
Matches 75; Conservative 27; Mismatches 26; Indels 4; Gaps 1;

OY 1 MKLPVRLVLLLEWIPVSGDVVVTQTPSLPVSFGDQVSIKRSQSLAKSYGNTYLSW 60
DB 1 METPAQLLFLLLLWLPDTTGIVLTQSPGTLSPGERATLSCRASQSVSS---YLAW 56
OY 61 YLHRPGSQPLLIIYGINRFSVDPDRFSGSGGTDFTLKISTIKPEDLGMVYCLOGTHOP 120
DB 57 YQKPGCAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVIYCCQYGTSP 116
OY 121 YTFGGGTKEIK 132
DB 117 YTFGGGTKEIK 128

RESULT 8
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR: PLO021; K3HUHI.
DR HSP: P01788; 2MCP.

InterPro: IPR003006; -.
Pfam: PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT DOMAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528E2BB74D6 CRC64;

Query Match 57.6%; Score 400; DB 1; Length 129;
Best Local Similarity 56.1%; Pred. No. 3.9e-33;
Matches 74; Conservative 28; Mismatches 26; Indels 4; Gaps 1;

OY 1 MKLPVRLVLLLEWIPVSGDVVVTQTPSLPVSFGDQVSIKRSQSLAKSYGNTYLSW 60
DB 1 METPAQLLFLLLLWLPDTTGIVLTQSPGTLSPGERATLSCRASQSVSS---YLAW 56
OY 61 YLHRPGSQPLLIIYGINRFSVDPDRFSGSGGTDFTLKISTIKPEDLGMVYCLOGTHOP 120
DB 57 YQKPGCAPRLIIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVIYCCQYGTSP 116
OY 121 YTFGGGTKEIK 132
DB 117 YTFGGGTKEIK 128

RESULT 9
KV2C_HUMAN STANDARD; PRT; 112 AA.
ID P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -!- MISCELLANEOUS: THE C-REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR: A01887; K2HUMI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; ig; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 56.9%; Score 395.5; DB 1; Length 112;
Best Local Similarity 65.2%; Pred. No. 9.3e-33;
Matches 73; Conservative 20; Mismatches 18; Indels 1; Gaps 1;
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SEQUENCE.
RP RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Blochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC PR: A01913; KWS7S.
DR InterPro: IPR0033006; -.
DR Pfam: PF000047; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT FT DOMAIN 40 54 FRAMEWORK 2.
FT FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT FT DOMAIN 62 93 FRAMEWORK 3.
FT FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT FT DOMAIN 103 112 FRAMEWORK 4.
FT FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 56.7%; Score 394; DB 1; Length 113;
Best Local Similarity 67.9%; Pred. No. 1.3e-32;
Matches 76; Conservative 14; Mismatches 22; Indels 0; Gaps

QY 21 DVVVQTPLSLPFGSDVISCRSSOSLAKSYNTLSWLVHKKPGSPOLLTYGTSNRF 80
I:L:I:L:I L: : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIVVTQTAPSNLYTPGESVSICRSKSLHSNGNYLYWFQRQCQPOLLIRYNSLA 60
I:L:I:L:I L: : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 81 SGVPDRSGSGGTDFTLTKTSTIKPEDLGMYCQLQTHGPYTFGGTGKLEIK 132
I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I
DB 61 SGVPDRSGSGGTAFTRLISRVEADVGYYVCMQREVPTYTFGGTGKLEIK 112
I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I I:I:I:I:I

RESULT 12
KV2E_MOUSE STANDARD; PRT; 113 AA.
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DD 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE-Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 23S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RT Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
CC PR: A01912; KWS17.
DR InterPro: IPR003306; -.
DR Pfam: PF000047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT FT DOMAIN 40 54 FRAMEWORK 2.
FT FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT FT DOMAIN 62 93 FRAMEWORK 3.
FT FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT FT DOMAIN 103 112 FRAMEWORK 4.

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FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 56.4%; Score 392; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 2.le-32;
Matches 75; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

QY 21 DVVVTQTLSPVSGDQVSIQSRSSQSLAKSGYNTYLSWYHKFGQSPOLLIIYGISNRF 80
DB 1 DLIVMTQAFNSPVTLGTSSASISCRSKSLHSHNGITYLWYWKFGQSPOLLIIYQMSNLA 60
QY 81 SGVPDRFSGSGTDFTLKISTIKPEDLGMYCLOGTHQPTFFGGGKLEIK 132
DB 61 SGVPDRFSGSGTDFTLRISRVEADGVYCAHNLELPYFFGGGKLEIK 112

RESULT 13
KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=1090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78234887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 11-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79015520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR InterPro: IPI003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 55.8%; Score 387.5; DB 1; Length 131;
Best Local Similarity 56.8%; Pred. No. 7e-32;
Matches 75; Conservative 11; Mismatches 26; Indels 0; Gaps 0;

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Matches 75; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSLPVSGDQVSIQSRSSQSLAKSGYNTYLSW 60
DB 1 METDTLLLVLLWVPGSTGNIVLTQSPASLAVALGQRATISCRASESY-DSYGNSEMH 59
QY 61 YLHKFGQSPOLLIIYGISNRFSGVPDRFSGSGTDFTLKISTIKPEDLGMYCLOGTHQ 120
DB 60 YQOKFCQPPKLLIYLASNLESGVPARFSGSGRTDFTLTIDPVEADDAATYYCQNNEDP 119
QY 121 YTFGGGKLEIK 132
DB 120 WTFGGGKLEIK 131

RESULT 14
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X02990; CAA26733.1; -.
DR PIR; A01905; K4HU17.
DR HSP; P01789; 2MCP.
DR InterPro: IPR003006; -.
DR Pfam; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 133 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 55.5%; Score 385.5; DB 1; Length 134;
Best Local Similarity 57.1%; Pred. No. 1.le-31;
Matches 76; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSLPVSGDQVSIQSRSSQSLAKSGYNTYLS 59

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Db      1  MVLQTVFISLLWISGVDIVMTQSPDSLAVSLGERATINCKSSQSIYSSDNKNYLA 60
QY      60  WYLHKPGSQPLLIIYGINRFSGVDPDRSGSGGDTFLKISTIRKPEDLGMYYCLOGTHQ 119
Db      61  WYQKPGQPKLLIYWASTRESGVDPDRSGSGGDTFLTISSLAQEDVAVYVCOQYVNL 120
QY      120  PYTFGGGTKLEIK 132
Db      121  PWTFGGQTKVEIK 133

RESULT 15
KV3K_HUMAN
ID  KV3K_HUMAN      STANDARD;          PRT;      128 AA.
AC  P06311.
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-JAN-1988 (Rel. 06, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86041852; PubMed=2997711;
RA  Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT  III."
RL  Nucleic Acids Res. 13:6499-6513(1985).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; Z00021; CAA77316.1; -
DR  PIR; A01899; K3HU41.
DR  InterPro; IPR003006; -
DR  Pfam; PF00047; 19; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL          1 20
FT  CHAIN           21 128
FT  DOMAIN          21 43
FT  DOMAIN          44 54
FT  DOMAIN          55 69
FT  DOMAIN          70 76
FT  DOMAIN          77 108
FT  DOMAIN          109 117
FT  DOMAIN          118 128
FT  DISULFID        43 108
FT  NON_TER         128 128
SQ  SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match      54.7%; Score 380.5; DB 1; Length 128;
Best Local Similarity 55.3%; Pred. No. 3.4e-31;
Matches 73; Conservative 26; Mismatches 28; Indels 5; Gaps 1;

QY      1  MKLPVRLVLLWIPVSGDVVVTQTPLSLPVSGQVSIKRSQSLAKSYGNTVLSW 60
Db      1  METPAQLLFLLLWLPDPTTGIVLTQSPGTLSPGESATLSCRASQSVSN-----LAW 55
QY      61  YLHKPGSQPLLIIYGINRFSGVDPDRSGSGGDTFLKISTIRKPEDLGMYYCLOGTHQ 120
Db      56  YQKRGQSPRLIIRDASSRANGIPDRFSGGSGDTFLTIISRLPEDFAVYVCOQYSTSP 115
QY      121  YTFGGGTKLEIK 132
Db      116  YTFGGGTKLEIK 127
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Search completed: April 13, 2001, 15:40:18
Job time: 271 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:39:52 ; Search time 56.51 Seconds
(without alignments)
273.782 Million cell updates/sec

Title: US-08-700-737-12
Perfect score: 695
Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPYFFGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	447	64.3	104	11 Q9JL82	Q9JL82 mus musculus
2	412.5	59.4	114	4 Q9UL80	Q9UL80 homo sapien
3	356	51.2	109	4 Q9UL78	Q9UL78 homo sapien
4	334.5	48.1	108	4 Q9UL77	Q9UL77 homo sapien
5	326.5	47.0	298	11 Q9QYF0	Q9QYF0 mus musculus
6	326	46.9	109	4 Q9UL86	Q9UL86 mus musculus
7	323.5	46.5	108	4 Q9UL70	Q9UL70 mus musculus
8	319.5	46.0	99	11 Q9JL74	Q9JL74 mus musculus
9	319.5	46.0	108	4 Q9UL79	Q9UL79 mus musculus
10	319.5	46.0	214	11 Q9JL85	Q9JL85 mus musculus
11	315	45.3	109	4 Q9UL85	Q9UL85 mus musculus
12	314.5	45.3	103	11 Q9JL80	Q9JL80 mus musculus
13	311.5	44.8	108	4 Q9UL83	Q9UL83 mus musculus
14	310	44.6	107	4 Q9UL81	Q9UL81 mus musculus
15	295	42.4	106	5 Q9U410	Q9U410 schistosoma
16	287.5	41.4	101	11 Q9JL78	Q9JL78 mus musculus
17	279.5	40.2	107	11 Q9JL84	Q9JL84 mus musculus
18	263.5	37.9	97	11 Q9JL76	Q9JL76 mus musculus
19	249.5	35.9	109	6 Q9NOW5	Q9NOW5 oryctolagus

20	227	32.7	107	4 Q9NSD6	Q9NSD6 homo sapien
21	209.5	30.1	130	4 Q9NP29	Q9NP29 homo sapien
22	206.5	29.7	107	4 Q9UL82	Q9UL82 homo sapien
23	148	21.3	509	11 Q9QX57	Q9QX57 mus musculus
24	148	21.3	513	11 P97797	P97797 mus musculus
25	146	21.0	509	11 Q9W907	Q9W907 mus musculus
26	137	19.7	509	11 Q9WTN4	Q9WTN4 mus musculus
27	132.5	19.1	168	4 Q9UQ56	Q9UQ56 homo sapien
28	132.5	19.1	246	4 Q9UQ55	Q9UQ55 homo sapien
29	126.5	18.2	123	11 Q61243	Q61243 mus musculus
30	125.5	18.1	210	6 P79336	P79336 felis silve
31	119.5	17.2	509	11 P97710	P97710 rattus norv
32	118.5	17.1	93	4 Q9UL76	Q9UL76 homo sapien
33	117	16.8	123	4 Q9UK13	Q9UK13 homo sapien
34	115.5	16.6	418	11 Q70426	Q70426 rattus norv
35	115.5	16.6	509	11 Q9QW15	Q9QW15 rattus norv
36	114	16.4	116	4 Q9UL89	Q9UL89 homo sapien
37	111	16.0	209	6 Q9XSM7	Q9XSM7 salmirl sci
38	110.5	15.9	285	11 Q9JME9	Q9JME9 mus musculus
39	110	15.8	200	4 Q95776	Q95776 homo sapien
40	108	15.5	235	6 Q9XSM6	Q9XSM6 salmirl sci
41	107	15.4	397	4 Q9Y4V0	Q9Y4V0 homo sapien
42	105	15.1	337	13 Q9IB02	Q9IB02 sphoeroides
43	104.5	15.0	401	6 Q98835	Q98835 cercopithec
44	104	15.0	334	13 Q9IB05	Q9IB05 sphoeroides
45	104	15.0	506	6 Q46632	Q46632 bos taurus

ALIGNMENTS

RESULT 1

Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206024; AAF69322.1;
FT NON_TER 1
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 64.3%; Score 447; DB 11; Length 104;
Best Local Similarity 80.8%; Pred. No. 4.3e-38;
Matches 84; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 29 LSLPVSGQDVSTSCRSSQSLAKSYNTYLSWYHLKPGSQPOLLYIGISNRFSGVDPDRS 88
Db 1 LSLPVSLGQASISCRSSQSLVHTNGTYLHWYLOKPGSQPKLLYKVSNRFSGVDPDRS 60
QY 89 GSGSGDFTLKISTIKPEDLGMVYCLQTHQPTFGGKLEIK 132
Db 61 GSGSGDFTLKISTIRVEADLGVYFCSTTHVPTFGGKLEIK 104

RESULT 2

Q9UL80 ID Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;

	Query Match	51.28;	Score	356.	DB	4:	Length	109;		
	Best Local Similarity	58.9%;	Pred. No.	7.6e-29;						
	Motifs	66;	Conservative	23;	Mismatches	19;	Indels	4;	Gaps	1;
Qy	21	DWVYIQ [*] PLSLPVGDDGVSSICRSQSLSKSYGNTYLSWLHLHPGGSPQLLIYGISNRF	80							
		::::: :	:	:	:	:	:	:	:	:
		: :	:	:	:	:	:	:	:	:
DB	1	EVLTVLTPGTLSLSPGERATSLCSRASQSVSS---	YLAWYQQRPQGAPRLLIYGASSRA	56						
		::: :	:	:	:	:	:	:	:	:

RESULT	5	
ID	Q9QYF0	PRELIMINARY; PRT: 298 AA.
ID	Q9QYF0	
AC	Q9QYF0;	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DC	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)
DE	CN 8 SCFV.	
DE	CN 8.	
GN	Mus musculus (Mouse).	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur	
OX	NCBI_TaxID=10090;	
OX	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BALB/C; TISSUE=SPLEEN;	
RA	Shinohara N., Demura T., Fukuda H.;	
RA	submitted Apr-1999 to the EMBL/GenBank/DBJ databases.	

[2]
RN SEQUENCE FROM N.A.
RP
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB036341; BAA88633.1; -
DR HSP: P01607; 1REI
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 47.0%; Score 326.5; DB 11; Length 298;
Best Local Similarity 53.5%; Pred. No. 2.5e-25;
Matches 61; Conservative 19; Mismatches 29; Indels 5; Gaps 1;

Qy 19 GGDVVVTPPLSPVSGDQVSTCRSSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGINR 78
Db 171 GSDIELTQSPASLSVGETVITCRASGNI-----HNYLAWYQKQKSPQLLIYNAKT 225
Qy 79 RESGVPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
Db 226 LADGVPSRFSGSGGTQVSLKINSLOPEDFGSYQCQHFWTPTTFGGGKLEIK 279

RESULT 6
Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
AC Q9UL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56284.1; -
DR HSP: P01789; IMCP.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 46.9%; Score 326; DB 4; Length 109;
Best Local Similarity 54.5%; Pred. No. 8.3e-26;
Matches 61; Conservative 25; Mismatches 22; Indels 4; Gaps 1;

Qy 21 DVVVTQPLSLPVSGDQVSTCRSSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGINR 80
Db 1 EIVLTQSPGTLSPFGERATLSRASQSVSSS---YLAWYQKQPGAPRELIYGTSSRA 56
Qy 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
Db 57 TGIPDRFSGSGSETDFTLTISRLPEFAVYICQYGGSSIFTFPGGKVDIK 108

RESULT 7
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -
DR HSP: P01607; 1REI
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 46.5%; Score 323.5; DB 4; Length 108;
Best Local Similarity 56.2%; Pred. No. 1.5e-25;
Matches 63; Conservative 17; Mismatches 27; Indels 5; Gaps 1;

Qy 21 DVVVTQPLSLPVSGDQVSTCRSSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGINR 80
Db 1 DIQMTQSPSSLSASVGRVTITCRASQGI-----SNYLAWYQKQPKVPSLIYAASTLQ 55
Qy 81 SGVPDRFSGSGGTDFTLKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
Db 56 SGVPSRFSGSGGTDFTLTISLPEDVATYICQYKNSAPRTFPGGKLEIK 107

RESULT 8
Q9JL74 PRELIMINARY; PRT; 99 AA.
ID Q9JL74
AC Q9JL74;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206032; AAF69330.1; -
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 10939 MW; 3B25D0E784533324 CRC64;

Query Match 46.0%; Score 319.5; DB 11; Length 99;
Best Local Similarity 59.8%; Pred. No. 3.4e-25;
Matches 61; Conservative 17; Mismatches 19; Indels 5; Gaps 1;

Qy 31 LPVSFGDQVSTCRSSQSLAKSYGNTYLSWYHLKPGQSPQLLIYGINRSGVPDRFSGS 90
Db 3 LLVSAGDRVTITCRASQSVSND-----VAVYQKQPGSPKLLIYASNRYTGVDPDRFTGS 57
Qy 91 GSGTDFTLTKISTIKPEDLGMVYCLQGTQHPYTFGGGKLEIK 132
Db 58 GYGTDFTTTQAEADLAVYFCQDYSSPRTFGGGKLEIK 99

RESULT 9
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79

Q9UL79;
 01-MAY-2000 (TReMBLrel. 13, Created)
 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035035; AAD56271.1; -.
 DR HSSP; P01607; IREI.
 DR INTERPRO; IPF003006; -.
 DR PFAM; PF00047; ig. 1.
 DR NON_TER 1
 FT NON_TER 108
 SQ SEQUENCE 168 AA; 11787 MW; DB5845F19724FB4E CRC64;
 Query Match 46.0%; Score 319.5; DB 4; Length 108;
 Best Local Similarity 57.1%; Pred. No. 3.8e-25;
 Matches 64; Conservative 15; Mismatches 28; Indels 5; Gaps 1;
 QY 21 DVVVQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQPOLLYIGISNRF 80
 Db 1 DIVVTQSPILLSASTGDRVTISCRMSQGI-----SSYLAWYQKPGKAPPELLIYAASTLQ 55
 QY 81 SGVPDRFSGSGGTDTFTLKISTIKPEDLGMVYCLQTHQPTFFGGGKLEIK 132
 Db 56 SGVPSRFSGSGGTDTFTLKISLQSEDFAITYYQQYSPFPPTFGGQTKVEIK 107
 RESULT 10
 Q9RIA5
 ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
 AC Q9RIA5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10990;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RA "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 antibody (Ma) 7, its light and heavy chains) and construction of a
 single chain antibody (scFv)".
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152371; AAD40242.1; -.
 DR HSSP; P01789; IMCP.
 DR INTERPRO; IP003006; -.
 DR PFAM; PF00047; ig. 2.
 DR PROSITE; PS02290; IG_MHC; UNKNOWN_1.
 DR NON_TER 1
 FT NON_TER 214
 SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
 Query Match 46.0%; Score 319.5; DB 11; Length 214;
 Best Local Similarity 52.7%; Pred. No. 8.6e-25;
 Matches 59; Conservative 24; Mismatches 24; Indels 5; Gaps 1;
 QY 21 DVVVQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQPOLLYIGISNRF 80

Db 1 DIQTFQSPSSMYASLGERVITTCASQDI-----NSYLSWFQKPGKSPKTLIYRANRLV 55
 QY 81 SGVPDRFSGSGGTDTFTLKISTIKPEDLGMVYCLQTHQPTFFGGGKLEIK 132
 Db 56 DGVPFRSGSGGSDYSLTSSLEVEDMGIIYCYLDYDFPFTFGSGTKLEIK 107
 RESULT 11
 Q9UL85
 ID Q9UL85 PRELIMINARY; PRT; 109 AA.
 AC Q9UL85;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -.
 DR HSSP; P01607; IREI.
 DR INTERPRO; IP003006; -.
 DR PFAM; PF00047; ig. 1.
 DR NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
 Query Match 45.3%; Score 315; DB 4; Length 109;
 Best Local Similarity 53.1%; Pred. No. 1.1e-24;
 Matches 60; Conservative 26; Mismatches 21; Indels 6; Gaps 2;
 QY 21 DVVVQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQPOLLYIGISNRF 80
 Db 1 EIVMTQSPATLSVSPGERATLSCWASQSISSN-----LAWYQKPGQAPRLIYGA STRA 55
 QY 81 SGVPDRFSGSGGTDTFTLKISTIKPEDLGMVYCLQ-GTHQPTFFGGGKLEIK 132
 Db 56 TGIPARFSGSGGTFTLTISSLSQSEDFAIYHCQQYNSWNPPLTFGGGKTKVEIK 108
 RESULT 12
 Q9JL80
 ID Q9JL80 PRELIMINARY; PRT; 103 AA.
 AC Q9JL80;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucoamine antibodies from mice with autoimmune myocarditis".
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF206026; AAF69324.1; -.
 DR NON_TER 1
 FT NON_TER 103
 SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:35:37 ; Search time 57.59 Seconds
(without alignments)
131.022 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLOGTHQPYFGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	695	100.0	132	19 W53814	Murine Act-1 light
2	695	100.0	140	19 W53817	Consensus protein
3	608	87.5	138	19 W53812	Light chain of a h
4	559.5	80.5	238	18 W14942	3F4 Human IgG4 exp
5	559.5	80.5	238	18 W14937	Murine anti-porcine
6	558.5	80.4	131	18 W34518	Variable kappa cha
7	554.5	79.8	149	17 W03199	Anti-idiotypic mono
8	554.5	79.8	149	20 Y21545	Monoclonal antibod
9	552.5	79.5	149	20 Y49209	MAB 1A7 light chai
10	552.5	79.5	149	20 Y28468	Light chain variab
11	550.5	79.2	131	21 B23812	Plasmid pGEM-MIL m

12	548.5	78.9	131	15 R52772	Murine KC-4 immuno
13	548.5	78.9	131	15 R52790	Murine KC-4 immuno
14	548.5	78.9	131	16 R70457	VL sequence of ant
15	546.5	78.6	238	20 Y17416	Mouse immunoglobul
16	543.5	78.2	131	14 R32241	Chimeric MAB light
17	543.5	78.2	131	14 R31587	BR55-2 light chain
18	537.5	77.3	131	14 R32245	BR55-2 murine IgG3
19	537.5	77.3	131	15 R52822	Humanised murine K
20	537.5	77.3	131	16 R70470	Humanised anti-KC-
21	535.5	77.1	132	19 W60867	Variable region of
22	535.5	77.1	132	21 Y80294	IgM chimeric antib
23	535.5	77.1	238	18 W31752	L chain subunit of
24	535.5	77.1	238	19 W71889	Anti-human Fas mon
25	535.5	77.1	238	21 B12909	Anti-human Fas ant
26	530.5	76.3	131	21 B23814	Plasmid pGEM-W2L m
27	529.5	76.2	140	19 W68492	Variable light cha
28	527.5	75.9	172	12 R15199	R6-S-D6 anti-ICAM-
29	523	75.3	150	12 R11598	Murine monoclonal
30	519.5	74.7	131	15 R52788	Murine BrE-3 immu
31	519.5	74.7	131	15 R52770	Murine BrE-3 immu
32	517.5	74.5	131	11 R09424	Co-1 Light Chain V
33	517.5	74.5	131	18 W06214	MAB Co-1 light cha
34	513	73.8	127	19 W78124	Murine ICR-8.1 V-K
35	513	73.8	127	19 W71254	Murine antibody IC
36	513	73.8	127	20 Y00781	Murine antibody IC
37	513	73.8	127	20 W81448	Antibody against I
38	513	73.8	127	21 B13044	Murine antibody IC
39	513	73.8	127	21 Y82443	Murine ICR-8.1 ant
40	513	73.8	127	21 Y50751	Murine antibody IC
41	511.5	73.6	131	15 R52806	Humanised murine B
42	511.5	73.6	131	20 W85060	Mouse Co-1 light c
43	509	73.2	132	19 W50219	Amino acid sequenc
44	506.5	72.9	173	12 R15059	Murine anti-ICAM m
45	503	72.4	239	19 W71876	Anti-human Fas hum

ALIGNMENTS

RESULT 1
W53814
ID W53814 standard; Protein; 132 AA.
XX
AC W53814;
XX
DT 14-JUL-1998 (first entry)
XX
DE Murine Act-1 light chain variable region.
XX
KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW humanised antibody; murine antigen binding region; inhibition;
KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW Inflammatory bowel disease.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /note= "signal peptide"
FT /note= "mature protein"
XX
XX W09806248-A2.
XX
XX
XX 19-FEB-1998.
XX
XX 06-AUG-1997; 97WO-US13884.
XX
XX 15-AUG-1996; 96US-0700737.
XX
XX (LEUK-) LEUKOSITE INC.
XX

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PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
PI Saldanha J;
XX WPI: 1998-159172/14.
XX N-PSDB; V2007.7.
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
XX used for treating inflammatory disease, pancreatitis, diabetes,
XX asthma, graft versus host disease and sarcoidosis
XX
XX Claim 23; Fig 7; 145pp; English.
XX
XX The present sequence represents the light chain variable region of
XX murine antibody Act-1. Act-1 is active against human alpha4-beta7
XX integrin. Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a
XX ligand of this particular integrin. The Act-1 antibody interferes with
XX alpha4-beta7 integrin binding to MacCAM-1, which is present of high
XX endothelial venules in mucosal lymph nodes. Humanised Act-1 can be used
XX to inhibit the interaction of cells bearing alpha4-beta7 with cells
XX bearing a ligand for alpha4-beta7. It can be used for inhibiting
XX leukocyte infiltration of tissues, e.g. for treating inflammatory
XX diseases such as inflammatory bowel disease. The immunoglobulin can
XX also be used for detection, isolation and diagnosis.
XX
XX Sequence 142 AA;
XX
XX Query Match 100.0%; Score 695; DB 19; Length 132;
XX Best Local Similarity 100.0%; Pred. No. 3e-48;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 mklpvrllvlllfpvsggdvvvtqtpslpslpsvsgdqvsgisrscssqslaksygnlyslw 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOGTHQP 120
DB 61 ylhkpggspqlliygisnrfsgvdpdrfsgsggtftlkistikpedlgmyyclgqthqp 120
QY 121 YTFGGGCKLEIK 132
DB 121 ytfgggckleik 132
XX
RESULT 2
W53817
ID W53817 standard; Protein; 140 AA.
XX
AC W53817;
XX
XX 14-JUL-1998 (first entry)
XX
XX Consensus protein sequence of the murine variable light chain region.
XX
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
XX Muscosal adressin cell adhesion molecule-1; MacCAM-1;
XX humanised antibody; murine antigen binding region; inhibition;
XX leukocyte infiltration of tissue; treatment; inflammatory disease;
XX inflammatory bowel disease.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..20 /note= "signal peptide"
XX Protein 21..140 /note= "mature protein"
XX
XX W09806248-A..
XX
XX 19-FEB-1998
XX
XX 06-AUG-1997 97WO-US13884.

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XX 15-AUG-1996; 96US-0700737.
XX (LEUK-) LEUKOSITE INC.
XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
XX Saldanha J;
XX WPI: 1998-159172/14.
XX N-PSDB; V20086.
XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
XX used for treating inflammatory disease, pancreatitis, diabetes,
XX asthma, graft versus host disease and sarcoidosis
XX
XX Example 1; Fig 3; 145pp; English.
XX
XX The present sequence represents the consensus amino acid sequence
XX comprising the variable region of murine Act-1 antibody determined from
XX several independent mouse light chain variable region clones. Act-1 is
XX active against human alpha4-beta7 integrin. Muscosal adressin cell
XX adhesion molecule-1 (MacCAM-1) is a ligand of this particular integrin.
XX The Act-1 antibody interferes with alpha4-beta7 integrin binding to
XX MacCAM-1, which is present of high endothelial venules in mucosal
XX lymph nodes. Variable regions were amplified from DNA encoding Act-1
XX using degenerate PCR primers V20083-84. The degeneracy of the PCR primers
XX produced several different sequences, of which the present sequence is a
XX consensus sequence. The present sequence was used to construct
XX chimeric, humanised Act-1 antibodies, which contain murine antigen
XX binding regions. The humanised immunoglobulin can be used to inhibit
XX the interaction of cells bearing alpha4-beta7 with cells bearing a
XX ligand for alpha4-beta7. It can be used for inhibiting leukocyte
XX infiltration of tissues, e.g. for treating inflammatory diseases such
XX as inflammatory bowel disease. The immunoglobulin can also be used for
XX detection, isolation and diagnosis.
XX
XX Sequence 140 AA;
XX
XX Query Match 100.0%; Score 695; DB 19; Length 140;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-48;
XX Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MKLPVRLVLLFWIPVSGGDVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
DB 1 mklpvrllvlllfpvsggdvvvtqtpslpslpsvsgdqvsgisrscssqslaksygnlyslw 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMYYCLOGTHQP 120
DB 61 ylhkpggspqlliygisnrfsgvdpdrfsgsggtftlkistikpedlgmyyclgqthqp 120
QY 121 YTFGGGCKLEIK 132
DB 121 ytfgggckleik 132
XX
RESULT 3
W53812
ID W53812 standard; Protein; 138 AA.
XX
AC W53812;
XX
XX 14-JUL-1998 (first entry)
XX
XX Light chain of a humanised murine Act-1 antibody.
XX
XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
XX Muscosal adressin cell adhesion molecule-1; MacCAM-1;
XX humanised antibody; murine antigen binding region; inhibition;
XX leukocyte infiltration of tissue; treatment; inflammatory disease;
XX inflammatory bowel disease.
XX
XX Synthetic.
OS

```

OS Mus sp.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT 1..20
 FT /note= "signal peptide"
 FT 21..138
 FT /note= "mature protein"
 XX
 PN WO9806248-A2.
 XX
 PN 19-FEB-1998.
 XX
 XX 06-AUG-1997; 97WO-US13884.
 XX
 PR 15-AUG-1996; 96US-0700737.
 XX
 PA (LEUK-) LEUKOSITE INC.
 XX
 PI Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX
 DR WPI: 1998-159172/14.
 DR N-PSDB; V20075.
 XX
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX
 PS Claim 15; Fig 12; 145pp; English.
 XX
 CC The present sequence represents the light chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MacCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MacCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 XX
 SQ Sequence 138 AA;
 Query Match 87.5%; Score 608; DB 19; Length 138;
 Best Local Similarity 87.1%; Pred. No. 2.4e-41;
 Matches 115; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSISSRSSQSLAKSYGNTYLSW 60
 Db 1 mkplvrllvllfwlpvsgdvvmvmtqpslslpvtgpeasiscrssqslaksgntylsw 60
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYYCLOGTHQP 120
 Db 61 ylkpgsqpqllyigisnrfsgvdpdrfsqsgsgtdftlkisrveaedgvyyclqgthqp 120
 QY 121 YTFGGGKLEIK 132
 Db 121 ytfgggkveik 132
 RESULT 4
 W14942
 ID W14942 standard; Protein; 238 AA.
 XX
 AC W14942;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE 3F4 Human IgG4 expression plasmid insert product (light chain).
 XX

KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 OS Mus sp.
 XX WO9711971-A1.
 PN 03-APR-1997.
 XX
 PD 27-SEP-1996; 96WO-US15575.
 XX
 PF 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 XX (ALEX-) ALEXION PHARM INC.
 XX
 XX Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;
 XX
 DR WPI: 1997-212855/19.
 DR N-PSDB; T62938.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 65-66; 105pp; English.
 XX
 CC Heavy chain (W14941) and light chain (W14942) sequences
 CC correspond to murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody 3F4 (see also W14937-38). They
 CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
 CC also T62938). A chimeric antibody specific for porcine VCAM can be
 CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 XX
 SQ Sequence 238 AA;
 Query Match 80.5%; Score 559.5; DB 18; Length 238;
 Best Local Similarity 81.1%; Pred. No. 3e-37;
 Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSISSRSSQSLAKSYGNTYLSW 60
 Db 1 mkplvrllv-lmfwpvsgdvvmvmtqpslslpvgdqsiscrssqslvhsngntylqw 59
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYYCLOGTHQP 120
 Db 60 ylkpgsqpqllyigisnrfsgvdpdrfsqsgsgtdftlkisrveaedlgvyfcsqstchp 119
 QY 121 YTFGGGKLEIK 132
 Db 120 ytfgggkkleik 131
 RESULT 5
 W14937
 ID W14937 standard; Protein; 238 AA.
 XX
 AC W14937;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE Murine anti-porcine VCAM 3F4 light chain.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX

RESULT 7
 W03199
 ID W03199 standard; Protein; 149 AA.
 XX
 AC W03199;
 XX
 DT 26-FEB-1997 (first entry)
 XX
 DE Anti-idiotypic monoclonal antibody 1A7 variable light chain.
 XX
 KW Murine; mouse; anti-idiotypic; monoclonal antibody; MAB; 1A7;
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma;
 KW vaccine; treatment; palliate; detection; diagnosis;
 KW recombinant production; purification; probe; primer; assay;
 KW amplification; gene therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /label= sig_peptide
 FT /note= "framework region 1"
 FT Region 43..58
 FT /note= "complementarity determining region 1"
 FT Region 59..73
 FT /note= "framework region 2"
 FT Region 74..80
 FT /note= "complementarity determining region 2"
 FT Region 81..112
 FT /note= "framework region 3"
 FT Region 113..121
 FT /note= "complementarity determining region 3"
 FT Region 122..131
 FT /note= "framework region 4"
 XX
 W09622373-A2.
 XX
 XX 25-JUL-1996.
 XX
 PF 17-JAN-1996; 96WO-US00882.
 XX
 PR 16-JAN-1996; 96US-0372676.
 PR 17-JAN-1995; 95US-0372676.
 XX
 PA (KENT) UNIV KENTUCKY.
 XX
 PI Chatterjee M, Chatterjee SK, Foon KA;
 XX
 DR WPI; 1996-354530/35.
 DR N-PSDB; T31332.
 XX
 PT Monoclonal antibody 1A7 and related polynucleotide(s) and
 PT polypeptide(s) - useful to treat or palliate a GD2-associated
 PT disease, e.g. melanoma and glioma
 XX
 PS Claim 8; Fig 1; 141pp; English.
 XX
 CC The present sequence is that of the murine anti-idiotypic monoclonal
 CC antibody (MAB) 1A7 variable light chain. MAB 1A7 was raised against
 CC the anti-ganglioside 2 (GD2) MAB 14G2a, which binds an unique
 CC epitope of GD2. As the glycosphingolipid GD2 is expressed at high
 CC density by human neuroectodermal tumours, e.g. malignant melanoma,
 CC neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma
 CC of the lung, MAB 1A7, or its cDNA can be used in a vaccine to treat
 CC or palliate such diseases. They can also be used to reduce the
 CC risk of recurrence of a clinically detectable tumour, and detect an
 CC anti-GD2 Ab bound to a tumour cell.
 CC MAB 1A7 overcomes immune tolerance and induces an immune response
 CC against GD2, which comprises anti-GD2 Ab (humoral response) and

CC GD2-specific cells (cellular response). It can be used to purify
 CC anti-1A7 (Ab3), anti-GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or
 CC anti-GD2 in a sample or measure the level of cellular anti-1A7 or
 CC anti-GD2 activity.
 CC The cDNA can be used in expression systems for 1A7 prodn., and in
 CC the prepn. of probes and primers to respectively assay for 1A7
 CC cDNA, and amplify desired polynucleotides for use in gene therapy.
 XX
 SQ Sequence 149 AA;
 Query Match 79.8%; Score 554.5; DB 17; Length 149;
 Best Local Similarity 79.5%; Pred. No. 4.6e-37;
 Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFLWIPVSGGVVVTQTPLSLPVSFGDQVSIQSRSSQSLAKSYGNTYLSW 60
 DB 1 mklpvrllv-lmfwlpassddvltmtqtpslpvsldgqasiscrssqqlvhangntylew 59
 QY 61 YLHKGQSPQLLIYGISNRFSGVDPDRFSGSGSGTDFTLKISTIKPEDLGMYYCLOGTHOP 120
 DB 60 YLQKPGGSPNLIYFVSNRFSGVDPDRFSGSGSGTDFTLKISTIKVEADIGVYVCFGGSHVP 119
 QY 121 YTFGGGTTKLEIK 132
 DB 120 wtfggggtkleik 131
 RESULT 8
 Y21545
 ID Y21545 standard; Protein; 149 AA.
 XX
 AC Y21545;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Monoclonal antibody 1A7 light chain variable region.
 KW Psoriasis; immunological response; anti-idiotypic antibody; glutate;
 KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;
 KW monoclonal antibody; 1A7.
 OS Unidentified.
 XX
 PN W09925380-A2.
 XX
 PD 27-MAY-1999.
 XX
 PF 17-NOV-1998; 98WO-US24607.
 XX
 PR 16-NOV-1998; 98US-0192838.
 PR 17-NOV-1997; 97US-0065774.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Chatterjee M, Foon KA;
 XX
 DR WPI; 1999-347407/29.
 DR N-PSDB; X60629.
 XX
 PT Treatment of psoriasis
 PS Disclosure; Fig 2; 48pp; English.
 CC The invention provides a method of treating of psoriasis by administering
 CC an antigen which has similar immunogenic properties to an antigen
 CC expressed on cells of psoriatic tissue so that an immunological response
 CC is elicited in the individual. The antigen stimulates the generation of
 CC anti-idiotypic antibodies that neutralize the aberrant immune response
 CC causing the psoriasis. The method is used to treat psoriasis, especially
 CC chronic plaque, glutate, pustular, plaque-type psoriasis or psoriatic
 CC arthritis. The compositions allow the individual's own immune system to
 CC act against psoriatic tissue. The present sequence represents the light


```

Query Match          78.9%; Score 548.5; DB 15; Length 131;
Best Local Similarity 78.8%; Pred. No. 1.2e-36;
Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

      y    1   MKLPLVRLVLLELFWIPVSQGDVVVTQTPLSLPVSFGDQVSISSCRSSQLAKSYGNTYLSW 60
      ||| |||| | : ||| |||| | ||| |||| | ||| |||| | ||| |||| | ||| |||| |
      y    1   mklplrvllv-lmfwlpasdsdvlmqtplsipvsjgqdasiscrssqsivhsngntylew 59
      ||| |||| | : ||| |||| | ||| |||| | ||| |||| | ||| |||| | ||| |||| |

      y    61  YLHKFCQPOLLIIYGISNRFSGVPPRRFSCGSGTDFTLKISTIKPEDLGMYXCLOGTHOP 120
      ||| |||| | : ||| |||| | ||| |||| | ||| |||| | ||| |||| | ||| |||| |
      y    60  Ylqkpgsqkllilyksvifrsfgvdpsgsdgtoftnlsrveadligiyvcfsgsnvp 119
      ||| |||| | : ||| |||| | ||| |||| | ||| |||| | ||| |||| | ||| |||| |

      y    121 YTFGGGTKLEIK 132
      ||| |||| | : ||| |||| | ||| |||| | ||| |||| | ||| |||| |
      y    120 Ytfgggtkleik 131
      ||| |||| | : ||| |||| | ||| |||| | ||| |||| | ||| |||| |

RESULT 14
70457
R70457 standard; Peptide; 131 AA.
X X R70457;

```

DT 27-OCT-1995 (first entry)
 XX VL sequence of anti-KC-4 monoclonal antibody (kII-Jk2).
 DE Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.
 XX Synthetic.
 KW WO9510776-A.
 XX 20-APR-1995.
 XX 16-NOV-1993; 93WO-US11444.
 PF 08-OCT-1993; 93US-0134346.
 XX (CANC-) CANCER RESEARCH FUND CONTRA COSTA.
 XX Ceriani RL, Docouto JJR, Peterson JA;
 PI WPI; 1995-161912/21.
 DR N-PSDB; Q87531.
 XX New humanised anti-KC-4 monoclonal antibody - used for detection of
 PT cancer cells, in vivo imaging, ex-vivo purging and treatment of
 PT cancers
 PT Example; Table 14, Page 31; 61pp; English.
 XX The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL
 CC were prepared by PCR from polyadenylated RNA isolated from 100
 CC million KC-4 hybridoma cells. All clones were obtd. from independent
 CC PCRs. The sequences of the primers are given in Q87519-Q87526.
 CC The PCR products were cloned, without prior purification, into pCR1000
 CC (Invitrogen) and sequenced in both directions. The VL DNA sequence and
 CC its derived protein sequences are shown in Q87531 and R70449-R70457.
 CC The mature VL chain begins at AA D of framework 1 (FR1). VL is a
 CC group II kappa chain. Part of the CDR3 and all of the FR4 are
 CC encoded by Jk2. There is an asparagine glycosylation site in the
 CC light chain in FR3. The site reads NIS. R70457 is a composite
 CC sequence of R70449-R70456.
 XX Sequence 131 AA;

Query Match 78.9%; Score 548.5; DB 16; Length 131;
 Best Local Similarity 78.8%; Pred. No. 1.2e-36;
 Matches 104; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFWIPVSGGVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 mklpvrliv-lmfwpasssdvmtqtplslpvsigdqasiscrssqslvhsngntylew 59
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGGTFTLKISTIKPEDLGMYCYLGQTHQP 120
 DB 60 ylkpgsqpklilykvsirfsgvdpdrfsgsggtftlnisrveadlgyycfcgshvp 119
 QY 121 YTFGGGTTKLEIK 132
 DB 120 ytfggggtkleik 131

RESULT 15
 Y17416
 ID Y17416 standard; Protein; 238 AA.
 AC Y17416;

DT 26-JUL-1999 (first entry)
 XX Mouse immunoglobulin E light chain.
 DE Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
 KW

XX Mus sp.
 OS Key
 XX Location/Qualifiers
 FH 1..19
 FT Peptide
 FT /label= signal
 FT 20..238
 FT /label= immunoglobulin_E_light_chain
 XX EP921189-A1.
 PN 09-JUN-1999.
 PD 13-NOV-1998; 98EP-0309340.
 XX 14-NOV-1997; 97JP-0313989.
 PR (SANY) SANKYO CO LTD.
 PA (TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
 XX Karasuyama H, Matsuoka K, Taya C, Yonemawa H;
 PI WPI; 1999-315404/27.
 DR N-PSDB; X61085.
 XX Transgenic non-human animal allergy models
 PT Claim 28; Page 30-32; 42pp; English.
 PS The present invention describes a transgenic, non-human animal with its
 CC genome altered to constitutively express a molecule having a constant
 CC region which can bind an IgE receptor on mast cells in the animals, the
 CC molecule having an immunoglobulin structure and being further capable of
 CC specifically binding a predetermined antigen. The transgenic animal is
 CC useful as a model for evaluating the activity and the ability of
 CC substances i.e. with anti-allergic activity, to affect any allergic
 CC reaction caused in the animal by the administration of the antigen to
 CC the animal, and applying the substance to be evaluated. The present
 CC sequence is the mouse immunoglobulin E (IgE) light chain, given in
 CC the present invention.
 XX Sequence 238 AA;

Query Match 78.6%; Score 546.5; DB 20; Length 238;
 Best Local Similarity 78.0%; Pred. No. 3.2e-36;
 Matches 103; Conservative 11; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLLFWIPVSGGVVVTQTPLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
 DB 1 mklpvrliv-lmfwpasssdvmtqtplslpvsigdqasiscrssqslvhsngntylew 59
 QY 61 YLHKPGSQPLLIIYGISNRFSGVDPDRFSGSGGTFTLKISTIKPEDLGMYCYLGQTHQP 120
 DB 60 ylkpgsqpklilykvsirfsgvdpdrfsgsggtftlkisrveadlgyycfcgshvp 119
 QY 121 YTFGGGTTKLEIK 132
 DB 120 ltfggggtkleik 131

Search completed: April 13, 2001, 15:35:39
 Job time: 118 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:55 ; Search time 4.45 Seconds
(without alignments)
51.491 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLLEWIPVSGG.....CLOGTHQPTFGGTXLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7695 seqs, 1735856 residues

Total number of hits satisfying chosen parameters: 7695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pap:*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pap:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pap:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pap:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pap:*
- 6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391.5	56.3	240	5	US-09-782-504-4
2	366.5	52.7	495	5	US-09-509-031-4
3	357.5	51.4	482	5	US-09-509-031-16
4	334.5	51.0	135	5	US-09-509-031-11
5	334.5	51.0	342	5	US-09-509-031-6
6	304	43.7	128	4	US-08-475-815A-7
7	303.5	43.7	109	5	US-09-386-658-4
8	101	14.5	140	4	US-08-475-815A-11
9	90.5	13.0	132	5	US-09-386-658-2
10	74	10.6	582	5	US-09-333-077-334
11	70.5	10.1	640	5	US-09-808-689-12
12	69.5	10.0	342	5	US-09-815-108-20
13	69.5	10.0	509	5	US-09-815-108-3
14	69.5	10.0	529	5	US-09-815-108-2
15	69.5	10.0	594	5	US-09-815-108-22
16	67.5	9.7	418	5	US-09-815-108-6
17	67.5	9.7	472	5	US-09-815-108-5
18	67.5	9.7	504	5	US-09-815-108-8
19	67.5	9.7	504	5	US-09-815-108-15
20	67.5	9.7	504	5	US-09-815-108-17
21	67.5	9.7	504	5	US-09-815-108-19
22	65	9.4	299	5	US-09-808-689-6
23	62.5	9.0	331	6	US-60-278-037-2
24	62.5	9.0	740	1	PCT-US01-09226-61
25	62.5	9.0	1250	1	PCT-US01-09226-62
26	62	8.9	312	5	US-09-808-689-2
27	61.5	8.8	2399	5	US-09-739-449-11472

28	60	8.6	680	5	US-09-739-449-11753	Sequence 11753, A
29	58	8.3	304	5	US-09-739-449-9355	Sequence 9355, Ap
30	57.5	8.3	209	5	US-09-739-449-11033	Sequence 11033, A
31	57.5	8.3	325	5	US-09-739-449-8751	Sequence 8751, Ap
32	57.5	8.3	574	5	US-09-815-108-7	Sequence 7, Appl
33	57	8.2	868	5	US-09-739-449-12606	Sequence 12606, A
34	56.5	8.1	427	5	US-09-739-449-10896	Sequence 10896, A
35	56.5	8.1	546	5	US-09-739-449-12091	Sequence 12091, A
36	56	8.1	550	5	US-09-739-449-9798	Sequence 9798, Ap
37	56	8.1	654	6	US-60-278-037-7	Sequence 7, Appl
38	55.5	8.0	1085	5	US-09-739-449-9734	Sequence 9734, Ap
39	55	7.9	299	5	US-09-809-391-396	Sequence 396, App
40	55	7.9	490	5	US-09-739-449-13176	Sequence 13176, A
41	54.5	7.8	176	5	US-09-739-449-10487	Sequence 10487, A
42	54	7.8	118	5	US-09-739-449-11965	Sequence 11965, A
43	54	7.8	385	5	US-09-739-449-9552	Sequence 9552, Ap
44	54	7.8	1059	5	US-09-808-689-10	Sequence 10, Appl
45	54	7.8	1119	5	US-09-808-689-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-782-504-4
; Sequence 4, Application US/09782504
; GENERAL INFORMATION:
; APPLICANT: Hellstrom, Ingegerd
; Bruce, Kim Folger
; Schreiber, George J.
; Siegall, Clay
; McAndrew, Stephen
; TITLE OF INVENTION: ANTIBODIES REACTIVE WITH HUMAN
; CARCINOMAS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,504
; FILING DATE: 12-Feb-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 840065.405D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-504-4

Query Match 56.3%; Score 391.5; DB 5; Length 240;
Best Local Similarity 70.6%; Pred. No. 9.1e-34;
Matches 84; Conservative 10; Mismatches 16; Indels 9; Gaps 6;

Query Match	51.0%;	Score 354.5;	DB 5;	Length 342;
Best Local Similarity	61.9%;	Pred. No. 7.8e-30;		


```

Db      55 HWFOQKSGSSPKPIYATSNLASGVPVRFSGSGGTSYSLTISRVEADAATYYCOOWTS 114
Qy      119 QPYTFGGGTKLEIK 132
           I | | | | | | | | |
Db      115 NPPTFGGGTKLEIK 128

RESULT 7
US-09-386-658--4
; Sequence 4, Application US/09386658
; GENERAL INFORMATION:
; APPLICANT: Erlanger, Bernard
; APPLICANT: Chen, Bi-Xing
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575-54182/JPW/SHS/MVM
; CURRENT APPLICATION NUMBER: US/09/386,658
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-09-386-658--4

Query Match          43.7%; Score 303.5; DB 5; Length 109;
Best Local Similarity 52.7%; Pred.No.3e-25;
Matches 59; Conservative 19; Mismatches 29; Indels 5; Gaps

Qy      21 DVVVOTPLSLPVFGDQVSISCRSSQSLAKSYGNTYLSWYLHKPQSPQLLIYGISNRF 80
           I : : : : I I I I : : : : I I I I I I : : : : I :
Db      1 DIQWTTSSLASLGRVTFSCASQDI-----NNYLNWYQQKPDGTIKKLIYYTSSLR 55
           I : : : : I I I I : : : : I I I I I I : : : : I :
Qy      81 SGVPDRFSGSGGTDFTLKISTIKPEDLGNYCYLCQTHOPYTFGGGGTKLEIK 132
           I I I I I I I I I I I I : : : : I I I : : : I I I I I I
Db      56 SGVPSRFRSGSGGTDSLINNLEPEDIATYFCQYSRLPFTFGSGTKLEIK 107
           I I I I I I I I I I I I : : : : I I I : : : I I I I I I

RESULT 8
US-08-475-815A-11
; Sequence 11, Application US/08475815A
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RES
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B C
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:

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RESULT 10-
US-09-533-077-331

Db • 120 AY-WGO3TLLTV 130

```
RESULT 12
US-09-815-108-20
; Sequence 20, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-815-108-20

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 342;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-PLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQPOLLIYGISNRFS 81
DB 217 VLTGTHPVNTTDFGTTSFQCK-----VRSDVKPVIQWL-----KRVEYSGEGRHN 263
QY 82 GVDP-----RFGSGSGTDF-----LKISTIKPEDLGMYYCLOGTHQPYTF 123
DB 264 STIDVGQKFVVLPTGVDWNSRDPDGYLNLKLLISRARQDDAGMYICLGANTMGYSF 318

RESULT 13
US-09-815-108-3
; Sequence 3, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (355)..(375)
US-09-815-108-3

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 509;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-PLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQPOLLIYGISNRFS 81
DB 223 VLTGTHPVNTTDFGTTSFQCK-----VRSDVKPVIQWL-----KRVEYSGEGRHN 269
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```
QY 82 GVDP-----RFGSGSGTDF-----LKISTIKPEDLGMYYCLOGTHQPYTF 123
DB 270 STIDVGQKFVVLPTGVDWNSRDPDGYLNLKLLISRARQDDAGMYICLGANTMGYSF 324

RESULT 14
US-09-815-108-2
; Sequence 2, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-815-108-2

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 529;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-PLSLPVSGDQVSISSCRSSQSLAKSYGNTYLSWYHLKPGSQPOLLIYGISNRFS 81
DB 243 VLTGTHPVNTTDFGTTSFQCK-----VRSDVKPVIQWL-----KRVEYSGEGRHN 289
QY 82 GVDP-----RFGSGSGTDF-----LKISTIKPEDLGMYYCLOGTHQPYTF 123
DB 290 STIDVGQKFVVLPTGVDWNSRDPDGYLNLKLLISRARQDDAGMYICLGANTMGYSF 344

RESULT 15
US-09-815-108-22
; Sequence 22, Application US/09815108
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/815.108
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: murine FGFR-L
; OTHER INFORMATION: extracellular domain-Fc fusion polypeptide
US-09-815-108-22

Query Match
Best Local Similarity 10.0%; Score 69.5; DB 5; Length 594;
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Best Local Similarity 24.3%; Pred. No. 1.2;
Matches 28; Conservative 16; Mismatches 44; Indels 27; Gaps 5;

QY 23 VVTQT-P.SLPVSFGDQVSTSCRSSOSLAKSYGNTYLSWYHKKPGGSPQLLIYGISNRFS 81

Db 243 VLTGTHP/NTTVDFGGTTSFOCK-----VRSDVKPVIQWL-----RVEYGESEGRHN 289

QY 82 GVPD---RFGSGSGTDFT-----LKISTIKPEDLGMYCYCQGTHQPYTF 123

Db 290 STIDVGG)KFEVLPDGDVWSRDPDGSYLNKLLISRARODDAGMYICLCGANTMGYSF 344

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Job time: 172 sec

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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:47 ; Search time 117.03 Seconds

(without alignments)

181.430 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence: 1 MKLPVRLVLLFWIPVSGG.....CLQGTHTQPTFGGKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
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- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	695	100.0	132	11 US-08-700-737-12	Sequence 12, Appl
2	695	100.0	140	11 US-08-700-737-6	Sequence 6, Appl
3	616	88.6	138	11 US-08-700-737-21	Sequence 21, Appl
4	593	85.3	112	11 US-08-700-737-7	Sequence 7, Appl
5	554.5	79.8	149	15 US-09-192-838-2	Sequence 2, Appl
6	554.5	79.8	149	17 US-09-324-191-2	Sequence 2, Appl
7	552.5	79.5	149	16 US-09-293-533-2	Sequence 2, Appl
8	550.5	79.2	131	19 US-09-523-095A-6	Sequence 6, Appl
9	537.5	77.3	131	5 US-08-134-346A-50	Sequence 50, Appl
10	537.5	77.3	131	13 US-08-976-288A-95	Sequence 95, Appl

11	536.5	77.2	131	8	US-08-485-044-4	Sequence 4, Appl
12	535.5	77.1	238	12	US-08-827-223-10	Sequence 10, Appl
13	535.5	77.1	238	12	US-08-827-223-10	Sequence 10, Appl
14	535.5	77.1	238	14	US-09-046-351-10	Sequence 10, Appl
15	530.5	76.3	131	19	US-09-523-095A-10	Sequence 10, Appl
16	527.5	75.9	173	3	US-07-946-313-3	Sequence 3, Appl
17	527.5	75.9	173	3	US-07-946-314-3	Sequence 3, Appl
18	527.5	75.9	173	10	US-08-650-108-3	Sequence 3, Appl
19	523.5	75.3	149	14	US-09-059-063-9	Sequence 9, Appl
20	519.5	74.7	131	3	US-07-977-706A-11	Sequence 11, Appl
21	519.5	74.7	131	3	US-07-977-706C-11	Sequence 11, Appl
22	519.5	74.7	131	3	US-07-977-707B-11	Sequence 11, Appl
23	519.5	74.7	131	5	US-08-128-015-11	Sequence 11, Appl
24	519.5	74.7	131	13	US-08-976-288A-11	Sequence 11, Appl
25	514	74.0	112	11	US-08-700-737-52	Sequence 52, Appl
26	513	73.8	127	6	US-08-286-754-45	Sequence 45, Appl
27	513	73.8	127	8	US-08-408-724-45	Sequence 45, Appl
28	513	73.8	127	8	US-08-472-819-45	Sequence 45, Appl
29	513	73.8	127	8	US-08-487-113C-45	Sequence 45, Appl
30	513	73.8	127	17	US-09-350-273-45	Sequence 45, Appl
31	513	73.8	127	17	US-09-382-289-45	Sequence 45, Appl
32	513	73.8	127	21	US-09-753-436-45	Sequence 78, Appl
33	503	72.4	239	14	US-09-046-351-78	Sequence 82, Appl
34	503	72.4	239	14	US-09-046-351-82	Sequence 82, Appl
35	500	71.9	129	12	US-08-827-223-82	Sequence 82, Appl
36	499	71.8	239	14	US-09-046-351-80	Sequence 80, Appl
37	499	71.8	239	14	US-09-046-351-84	Sequence 84, Appl
38	492.5	70.9	113	11	US-08-700-737-50	Sequence 50, Appl
39	492	70.8	263	16	US-09-293-533-66	Sequence 66, Appl
40	492	70.8	285	17	US-09-318-661-4	Sequence 4, Appl
41	488.5	70.3	219	5	US-08-155-874A-60	Sequence 60, Appl
42	488.5	70.3	219	10	US-08-665-839A-60	Sequence 60, Appl
43	488.5	70.3	219	10	US-08-665-839B-60	Sequence 60, Appl
44	488.5	70.3	219	10	US-08-665-839B-60	Sequence 60, Appl
45	488	70.2	219	18	US-09-454-925A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-700-737-12

: Sequence 12, Application US/08700737

: GENERAL INFORMATION:

: APPLICANT: Ponath, Paul D.

: APPLICANT: Ringler, Douglas J.

: APPLICANT: Jones, S. Tarran

: APPLICANT: Newman, Walter

: APPLICANT: Saldanha, Jos

: APPLICANT: Bendig, Mary M.

: TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7

: NUMBER OF SEQUENCES: 63

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

: STREET: Two Militia Drive

: CITY: Lexington

: STATE: Massachusetts

: COUNTRY: USA

: ZIP: 02173

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/700,737

: FILING DATE: 15-AUG-1996

: CLASSIFICATION: 435

: ATTORNEY/AGENT INFORMATION:

: NAME: Brook, David E.

: REGISTRATION NUMBER: 22,592

: REFERENCE/DOCKET NUMBER: LKS95-10

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-12

Query Match 100.0%; Score 695; DB 11; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.3e-61;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSFGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSFGDQVSIICRSQSLAKSYGNTYLSW 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTLTKISTIKPEDLGMYYCLOGTHOP 120
DB 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTLTKISTIKPEDLGMYYCLOGTHOP 120
QY 121 YTFGGGTRLEIK 132
DB 121 YTFGGGTRLEIK 132

RESULT 3
US-08-700-737-21
; Sequence 21, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brock, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-21

Query Match 88.6%; Score 616; DB 11; Length 138;
Best Local Similarity 87.9%; Pred. No. 2.4e-53;
Matches 116; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSFGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSFGDQVSIICRSQSLAKSYGNTYLSW 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTLTKISTIKPEDLGMYYCLOGTHOP 120
DB 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTLTKISTIKPEDLGMYYCLOGTHOP 120
QY 121 YTFGGGTRLEIK 132
DB 121 YTFGGGTRLEIK 132

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-12

Query Match 100.0%; Score 695; DB 11; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.3e-61;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSFGDQVSIICRSQSLAKSYGNTYLSW 60
DB 1 MKLPVRLVLLFWIPVSGDGVVVTQTPLSLPVSFGDQVSIICRSQSLAKSYGNTYLSW 60
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTLTKISTIKPEDLGMYYCLOGTHOP 120
DB 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTLTKISTIKPEDLGMYYCLOGTHOP 120
QY 121 YTFGGGTRLEIK 132
DB 121 YTFGGGTRLEIK 132

RESULT 2
US-08-700-737-6
; Sequence 6, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brock, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-700-737-6
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Db 61 YLOKPGSPQLLIYGISNRFSGVDPDRFSGSGCTDTLTKISRVEADGVVYICLQGTQHP 120
QY 121 YTFGGGTTKLEIK 132
Db 121 YTFGGGTTKVEIK 132

RESULT 4

US-08-700-737-7
; Sequence 7, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-700-737-7

Query Match 85.3%; Score 593; DB 11; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 DVVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWLHKPGQSPQLLIYGISNRF 80
Db 1 DVVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSWLHKPGQSPQLLIYGISNRF 60
QY 81 SCVDPDRFSGSGCTDTLTKISTIRPEDLGMYCICLQGTQHPYTFGGGTTKLEIK 132
Db 61 SCVDPDRFSGSGCTDTLTKISTIRPEDLGMYCICLQGTQHPYTFGGGTTKLEIK 112

RESULT 5

US-09-192-838-2
; Sequence 2, Application US/09192838
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000500

; CURRENT APPLICATION NUMBER: US/09/192,838
; CURRENT FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-192-838-2

Query Match 79.8%; Score 554.5; DB 15; Length 149;
Best Local Similarity 79.5%; Pred. No. 3.2e-47;
Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLLFWIPVSGDQVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFWIPASSDDVLMTQTPLSLPVSILGDAQSISCRSSQSIHVSNGNTYLEW 59
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGCTDTLTKISTIKRPEDLGMYCICLQGTQHP 120
Db 60 YLOKPGQSPNLLIYFVSNRFSQVDPDRFSGSGCTDTLTKISRVEADLGYYICFQGSHPV 119
QY 121 YTFGGGTTKLEIK 132
Db 120 WTEGGGTTKLEIK 131

RESULT 6

US-09-324-191-2
; Sequence 2, Application US/09324191
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
; APPLICANT: CHATTERJEE, Malaya
; APPLICANT: FOON, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000540
; CURRENT APPLICATION NUMBER: US/09/324,191
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: 60/065,774
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-324-191-2

Query Match 79.8%; Score 554.5; DB 17; Length 149;
Best Local Similarity 79.5%; Pred. No. 3.2e-47;
Matches 105; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLLFWIPVSGDQVVTQTPLSLPVSFGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFWIPASSDDVLMTQTPLSLPVSILGDAQSISCRSSQSIHVSNGNTYLEW 59
QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGCTDTLTKISTIKRPEDLGMYCICLQGTQHP 120
Db 60 YLOKPGQSPNLLIYFVSNRFSQVDPDRFSGSGCTDTLTKISRVEADLGYYICFQGSHPV 119
QY 121 YTFGGGTTKLEIK 132
Db 120 WTEGGGTTKLEIK 131

RESULT 7

US-09-293-533-2
; Sequence 2, Application US/09293533
; GENERAL INFORMATION:

```

; APPLICANT: Chatterjee, Malaya
; APPLICANT: Moon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 735 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-293-533-2

Query Match 79.5%; Score 552.5; DB 16; Length 149;
Best Local Similarity 79.5%; Pred. No. 5.1e-47;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MKLPVRLVLLFWIPVSGGDVVVTQPLSLPVSGDQVSIQSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFVIPASSDDVFMVTQPLSLPVSLGDAQSIQSCRSSQSIYHSNGNTYLEW 59

Qy 61 YLHKPGKSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMVYCLOGTHQP 120
Db 60 YLQKPGKSPNLLIYFVSNRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 119

Qy 121 YTFGGGKLEIK 132
Db 120 YTFGGGKLEIK 131

RESULT 8
US-09-523-095A-6
; Sequence 6, Application US/09523095A
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: UHO, Shinsuke
; APPLICANT: OHI-EDA, Masayoshi
; APPLICANT: KUCHI, Yasufumi
; TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN FV
; FILE REFERENCE: 065678/0102
; CURRENT APPLICATION NUMBER: US/09/523,095A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 11-63557
; PRIOR FILING DATE: 1999-03-10

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; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-523-095A-6

Query Match 79.2%; Score 550.5; DB 19; Length 131;
Best Local Similarity 80.3%; Pred. No. 7e-47;
Matches 106; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MKLPVRLVLLFWIPVSGGDVVVTQPLSLPVSGDQVSIQSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFVIPASSDDVFMVTQPLSLPVSLGDAQSIQSCRSSQSLHSGKNTYLOM 59

Qy 61 YLHKPGKSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISTIKPEDLGMVYCLOGTHQP 120
Db 60 YLQKPGKSPKLLIYKVSNRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVP 119

Qy 121 YTFGGGKLEIK 132
Db 120 YTFGGGKLEIK 131

RESULT 9
US-08-134-346A-50
; Sequence 50, Application US/08134346A
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-134-346A-50

Query Match 77.3%; Score 537.5; DB 5; Length 131;
Best Local Similarity 77.3%; Pred. No. 1.4e-45;
Matches 102; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

```


APPLICANT: Serizawa, Nobufusa
APPLICANT: Nakahara, Kaori
APPLICANT: Chikawa, Kimihisa
APPLICANT: Yonehara, Shin
TITLE OF INVENTION: ANTI-Fas RECOMBINANT ANTIBODIES AND DNA THEREFOR
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frishaut, Holtz, Goodman, Langer & Chick,
STREET: 767 Third Avenue
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10017-2023
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,223
FILING DATE: 27-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP Hei 8-78570
FILING DATE: 01-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Herbert
REGISTRATION NUMBER: 17081
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-319-4900
TELEFAX: 212-319-5101
TELEX: 236268
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-827-223-10

Query Match 77.1%; Score 535.5; DB 12; Length 238;
Best Local Similarity 78.0%; Pred. No. 4.2e-45;
Matches 103; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIISCRSSQSLAKSYGNTYLSW 60
||||| :||| :|||:||||| ||| |||||:| | |||||
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQSPSLPVSLGDAQASISCRSSKSLVHNSGNTYLHW 59
||||| :||| :|||:||||| ||| |||||:| | |||||

QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMVYCLOGTHOP 120
|| |||||:|||| :||||| ||||| ||||| |||||:| | |||||
DB 60 YLQKPGQSPKLLIYKVSINRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
|| |||||:|||| :||||| ||||| ||||| |||||:| | |||||

QY 121 YTFGGGKLEIK 132
|||||
DB 120 PAFGGGKLEIK 131
|||||

RESULT 13
US-08-827-223-10
; Sequence 10, Application US/08827223A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Nakahara, Kaori
; APPLICANT: Chikawa, Kimihisa
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: ANTI-Fas RECOMBINANT ANTIBODIES AND DNA THEREFOR
; FILE REFERENCE: 970093/HG
; CURRENT APPLICATION NUMBER: US/08/827,223A
; CURRENT FILING DATE: 1998-07-23
; EARLIER FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: JP Hei 8-78570
; EARLIER FILING DATE: 1996-04-01

NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-827-223-10

Query Match 77.1%; Score 535.5; DB 12; Length 238;
Best Local Similarity 78.0%; Pred. No. 4.2e-45;
Matches 103; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIISCRSSQSLAKSYGNTYLSW 60
||||| :||| :|||:||||| ||| |||||:| | |||||
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQSPSLPVSLGDAQASISCRSSKSLVHNSGNTYLHW 59
||||| :||| :|||:||||| ||| |||||:| | |||||

QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMVYCLOGTHOP 120
|| |||||:|||| :||||| ||||| ||||| |||||:| | |||||
DB 60 YLQKPGQSPKLLIYKVSINRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
|| |||||:|||| :||||| ||||| ||||| |||||:| | |||||

QY 121 YTFGGGKLEIK 132
|||||
DB 120 PAFGGGKLEIK 131
|||||

RESULT 14
US-09-046-351-10
; Sequence 10, Application US/09046351A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Takahashi, Tohru
; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-046-351-10

Query Match 77.1%; Score 535.5; DB 14; Length 238;
Best Local Similarity 78.0%; Pred. No. 4.2e-45;
Matches 103; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIISCRSSQSLAKSYGNTYLSW 60
||||| :||| :|||:||||| ||| |||||:| | |||||
DB 1 MKLPVRLV-LMFVIPASSSDVVMVTQSPSLPVSLGDAQASISCRSSKSLVHNSGNTYLHW 59
||||| :||| :|||:||||| ||| |||||:| | |||||

QY 61 YLHKPGQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFLKISTIKPEDLGMVYCLOGTHOP 120
|| |||||:|||| :||||| ||||| ||||| |||||:| | |||||
DB 60 YLQKPGQSPKLLIYKVSINRFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQSSTHVP 119
|| |||||:|||| :||||| ||||| ||||| |||||:| | |||||

QY 121 YTFGGGKLEIK 132
|||||
DB 120 PAFGGGKLEIK 131
|||||

RESULT 15
US-09-523-095A-10
; Sequence 10, Application US/09523095A
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: UNO, Shinsuke

; APPLICANT: OH-EDA, Masayoshi
; APPLICANT: KIKUCHI, Yasufumi
; TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN Fv
; FILE REFERENCE: 065678/0102
; CURRENT APPLICATION NUMBER: US/09/523,095A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 11-63557
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-523-095A-10

Query Match 76.3%; Score 530.5; DB 19; Length 131;
Best Local Similarity 78.0%; Pred. No. 6.7e-45;
Matches 103; Conservative 9; Mismatches 19; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLVLPVSGDVVYTOPPLSLPVSGDQVSIQSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFVPGSSDVVMTQSPVSLPVSLGDAQSIQSSQSLVHNSNGKTYLHW 59
QY 61 YLHRPGSQPLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYCYCQGTHOP 120
Db 60 YLQKPGSPKLLIYKVNRFSGVDPDRFSGSGSVTDFTLMSRVEAEDLGVIYFCQSQTHVP 119
QY 121 YTFGGGKLEIK 132
Db 120 YTFGGGKLEIK 131

Search completed: April 13, 2001, 17:37:49
Job time: 166 sec



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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:36:09 ; Search time 28.17 seconds
(without alignments)

90.019 Million cell updates/sec

Title: US-08-700-737-12

Perfect score: 695

Sequence:

1 MKLPVRLVLLFWIPVSGG.....CLOCTHOPYTFGGTKLEIK 132

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Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*

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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558.5	80.4	131	3	US-08-589-939-7
2	552.5	79.5	149	2	US-08-752-844-2
3	552.5	79.5	149	2	US-08-591-196-2
4	546.5	78.6	238	4	US-08-182-545-4
5	543.5	78.2	131	1	US-08-053-171-5
6	543.5	78.2	131	1	US-08-053-171-9
7	537.5	77.3	131	1	US-08-129-9308-95
8	527.5	75.9	173	5	PCT-US91-02942-3
9	527.5	75.9	173	5	PCT-US91-02946-3
10	519.5	74.7	131	1	US-07-977-696C-11
11	519.5	74.7	131	1	US-08-129-9308-11
12	513	73.8	127	1	US-08-482-882-45
13	513	73.8	127	2	US-08-483-389-45
14	513	73.8	127	2	US-08-487-113D-45
15	513	73.8	127	2	US-08-473-503-45
16	513	73.8	127	2	US-08-483-932-45
17	513	73.8	127	2	US-08-720-420A-45
18	513	73.8	127	3	US-08-714-017-45
19	513	73.8	127	3	US-08-475-680-45
20	492	70.8	263	2	US-08-752-844-66
21	485	69.8	135	1	US-08-259-372A-12
22	485	69.8	135	1	US-08-468-671-12
23	483	69.5	125	1	US-08-331-398A-67
24	483	69.5	125	2	US-08-331-397B-67
25	483	69.5	125	2	US-08-759-804A-66
26	481	69.2	110	1	US-08-244-626-2
27	481	69.2	238	2	US-08-224-591-12

28	481	69.2	238	2	US-08-392-338A-21	Sequence 21, Appl
29	481	69.2	238	2	US-08-926-789-12	Sequence 12, Appl
30	481	69.2	238	3	US-09-166-750-21	Sequence 21, Appl
31	481	69.2	238	3	US-09-166-093-21	Sequence 21, Appl
32	481	69.2	238	3	US-09-172-019-21	Sequence 21, Appl
33	481	69.2	238	4	US-09-166-094-21	Sequence 21, Appl
34	481	69.2	239	5	PCT-US93-11138-12	Sequence 12, Appl
35	481	69.2	240	2	US-08-392-338A-11	Sequence 11, Appl
36	481	69.2	240	3	US-09-166-750-11	Sequence 11, Appl
37	481	69.2	240	3	US-09-166-093-11	Sequence 11, Appl
38	481	69.2	240	3	US-09-172-019-11	Sequence 11, Appl
39	481	69.2	240	4	US-09-166-094-11	Sequence 11, Appl
40	481	69.2	246	1	US-08-237-341-7	Sequence 11, Appl
41	481	69.2	250	2	US-08-392-338A-15	Sequence 15, Appl
42	481	69.2	250	3	US-09-166-750-15	Sequence 15, Appl
43	481	69.2	250	3	US-09-166-093-15	Sequence 15, Appl
44	481	69.2	250	3	US-09-172-019-15	Sequence 15, Appl
45	481	69.2	250	4	US-09-166-094-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-589-939-7
; Sequence 7, Application US/08589939
; Patent No. 6015662
; GENERAL INFORMATION:
; APPLICANT: Hackett, Jr., John R.
; APPLICANT: Hoff, Jane A.
; APPLICANT: Ostrow, David H.
; APPLICANT: Golden, Alan M.
; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
; TITLE OF INVENTION: CONTROLS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,939
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5865.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-589-939-7

Query Match 80.4%; Score 558.5; DB 3; Length 131;
Best Local Similarity 81.1%; Pred. No. 3.4e-47;
Matches 107; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFWIPVSGDVVVVTTPLSLPVSFGDQVVISCRSSQSLAKSYGNTYLSW 60

Sat Apr 14 08:10:17 2001

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Db 1 MKLPVRLV-LMFVIPASSDDVMTQTLPLSPVSGDQASISCRSSQSLVHSYNGNTYLSW 59
QY 61 YLHKPGQSPOLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYCLOQTHOP 120
Db 60 YLQKPGQSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLGYYFCQSOSTHVP 119
QY 121 YTFGGGTLEIK 132
Db 120 WTEGGGTLEIK 131

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RESULT 2
US-08-752-844-2
; Sequence 2, Application US/08752844
; Patent No. 5935121
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 705141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-752-844-2

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Query Match 79.5%; Score 552.5; DB 2; Length 149;
Best Local Similarity 79.5%; Pred. No. 1.5e-46;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFVWIPVSGDQVVTQTLPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFVIPASSDDVMTQTLPLSLPVLGDAQSISCRSSQSIHVSNGNTYLSW 59
QY 61 YLHKPGQSPOLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYCLOQTHOP 120
Db 60 YLQKPGQSPNLLIYFVSNRFSGVDPDRFSGSGGTDFTLKISRVEADLGYYFCQSHVP 119
QY 121 YTFGGGTLEIK 132
Db 120 WTEGGGTLEIK 131

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RESULT 3
US-08-591-196-2
; Sequence 2, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-591-196-2

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Query Match 79.5%; Score 552.5; DB 2; Length 149;
Best Local Similarity 79.5%; Pred. No. 1.5e-46;
Matches 105; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 1 MKLPVRLVLLFVWIPVSGDQVVTQTLPLSPVSGDQVSISSCRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLV-LMFVIPASSDDVMTQTLPLSLPVLGDAQSISCRSSQSIHVSNGNTYLSW 59
QY 61 YLHKPGQSPOLLIIYGISNRFSGVDPDRFSGSGGTDFTLKISTIKPEDLGMYCLOQTHOP 120
Db 60 YLQKPGQSPNLLIYFVSNRFSGVDPDRFSGSGGTDFTLKISRVEADLGYYFCQSHVP 119
QY 121 YTFGGGTLEIK 132
Db 120 WTEGGGTLEIK 131

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RESULT 4
US-09-192-545-4
; Sequence 4, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 79979570
; CURRENT APPLICATION NUMBER: US/09/192,545

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MATCHES 103; **Conservative** 11; **Mismatches** 17; **Indels** 1

Matches 103; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

US-08-129-930B-95

US-08-129-930B-95

US-08-129-930B-95

APPLICATION NUMBER: PCT/US91/02946
FILING DATE: 19910429
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0576600
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02946-3

Query Match 75.9%; Score 527.5; DB 5; Length 173;
Best Local Similarity 77.3%; Pred. No. 4.7e-44;
Matches 102; Conservative 10; Mismatches 19; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSSQSLAKSYGNTYLSW 59
QY 61 YLHKPQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISIRVEADLGVTFCQSTHVP 120
Db 60 YLQKSCQAPKLLIYRASNRFSGVDPDRFSGSGGTDTFTLKISIRVEADLGVTFCQSTHVP 119
QY 121 YTFGGTKLEIK 132
Db 120 LTFGGTKLEIK 131

RESULT 10
US-07-977-696C-11
Sequence 11, Application US/07977696C
Patent No. 5792852
GENERAL INFORMATION:
APPLICANT: do Couto, Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides with Specificity
TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
TITLE OF INVENTION: and Therapeutic Methods.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,696C
FILING DATE: 11-16-92
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38227
TELEPHONE: (510) 748-6868
TELEFAX: (510) 748-6688
TELEX: n.a.

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-696C-11

Query Match 74.7%; Score 519.5; DB 1; Length 131;
Best Local Similarity 77.3%; Pred. No. 2e-43;
Matches 102; Conservative 10; Mismatches 19; Indels 1; Gaps 1;
QY 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSSQSLAKSYGNTYLSW 60
Db 1 MKLPVRLVLLFWIPVSGDVVVTQTPLSLPVSGDQVSIICRSSQSLAKSYGNTYLSW 59
QY 61 YLHKPQSPQLLIYGISNRFSGVDPDRFSGSGGTDTFTLKISIRVEADLGVTFCQSTHVP 120
Db 60 YLQKSCQAPKLLIYRASNRFSGVDPDRFSGSGGTDTFTLKISIRVEADLGVTFCQSTHVP 119
QY 121 YTFGGTKLEIK 132
Db 120 WTFGGTKLEIK 131

RESULT 11
US-08-129-930B-11
Sequence 11, Application US/08129930B
Patent No. 5804187
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. AMZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Amzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-129-930B-11

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Query Match          74.7%; Score 519.5; DB 1; Length 131;
Best Local Similarity 77.3%; Pred. No. 2e-43;
Matches 102; Conservative 10; Mismatches 19; Indels 1; Gaps 1;

DDB
1 MKLPVRLIVLLFWIPYSGGVVVVTPPLSLPVSGDQVSISSRSQSLSAKSYGNTYLSW 60
||||| ||||| |||:||||||| ||| |||||:| : |||||
1 MKLPVRLIV-LLEFWIPASISDVVMTPTPLSLPVSLGDAQISICRSQNIVHNNGNTYLYW 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY
61 YLHPGQS:POLLIYIGSNRRSGVDPDRSGSGSTGDTFLTKISTIKPDLGMWYCLQCTHOP 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DDB
60 FLQSGQS:PKLLIYTPASIRISGVDPDRSGSGSETDFTLKISRVEADLGVYFCQGTHTP 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY
121 YTFGGGTILEIK 132
:||||| ||||
DDB
120 WTFGGGTILEIK 131
:||||| ||||

RESULT 12
US-08-482-882-45
; Sequence 45, Application US/08482882
; Patent No. 5773:18
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: 'azeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6100 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60605
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,882
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5773218and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: am: no acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

```

MOLECULE TYPE: protein
US-08-483-389-45

Query Match 73.8%; Score 513; DB 2; Length 127;
Best Local Similarity 78.1%; Pred. No. 8.3e-43;
Matches 100; Conservative 9; Mismatches 17; Indels 2; Gaps 2;
QY 6 RLLVLLFWIPVSGDVVVTOTPLSLPVSGDOVSISCRSSQSLAKSYGNTYLSWYLRKP 65
DB 1 RLLV-LMXWIPVSSDAVMTOTPLSLPVSLGDAQASISCRSSQSLVHNSGDTYLRHWYLRKP 59
QY 66 GSPQLLIYGISNRFSGVDPDRF-SGSGSGTDTFTLKISTIKPEDLGNYCLOGTHQPTTFG 124
DB 60 GSPQLLIYKVSNRFGVDPDRFGSGSGTDTFTLKLSRVEADLGVYFCQSQTHVPYTFG 119
QY 125 GGTKLEIK 132
DB 120 GGTKLEIK 127

RESULT 14

US-08-487-113D-45
; Sequence 45, Application US/08487113D
; Patent No. 5837822
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,113D
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5837822and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-113D-45

Query Match 73.8%; Score 513; DB 2; Length 127;
Best Local Similarity 78.1%; Pred. No. 8.3e-43;
Matches 100; Conservative 9; Mismatches 17; Indels 2; Gaps 2;
QY 6 RLLVLLFWIPVSGDVVVTOTPLSLPVSGDOVSISCRSSQSLAKSYGNTYLSWYLRKP 65
DB 1 RLLV-LMXWIPVSSDAVMTOTPLSLPVSLGDAQASISCRSSQSLVHNSGDTYLRHWYLRKP 59
QY 66 GSPQLLIYGISNRFSGVDPDRF-SGSGSGTDTFTLKISTIKPEDLGNYCLOGTHQPTTFG 124
DB 60 GSPQLLIYKVSNRFGVDPDRFGSGSGTDTFTLKLSRVEADLGVYFCQSQTHVPYTFG 119
QY 125 GGTKLEIK 132
DB 120 GGTKLEIK 127

RESULT 15

US-08-473-503-45
; Sequence 45, Application US/08473503
; Patent No. 5869262
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5869262and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300

us-08-700-737-12.ra

Sat Apr 14 08:10:17 2001

```

; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-473-503-45

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Query Match      73.8%; Score 513; DB 2; Length 127;
Best Local Similarity 78.1%; Pred. No. 8.3e-43;
Matches 100; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

QY 6 RLIVLLWIPVSGDVVVTQTPLSLPVSGDQVSIICRSQSQSLAKSYGNTYLSWYLHKP 65
Db 1 RLLV-LM.WIPVSSDAVMTQTPLSLPVSLGDAQSICRSQSQSLVHNSGDTYLVHWYLOKP 59

QY 66 GQSPQLLYGINSNRFGVPDRF-SGSGSGTDFTLKISTIKPEDLGMYYCLOGTHOPYTFG 124
Db 60 GQSPQLLYKVSNRFGVPDRFSGSGSGTDFTLKLSRVEADLVGYFCQSTHVPYTFG 119

QY 125 GGTKLEIK 132
Db 120 GGTKLEIK 127

```

Search completed: April 13, 2001, 15:36:11
Job time: 129 sec

Result No.	Query No.	Score	Query		Length	DB	ID	Description
			Match	%				
1	1	603	79.7	138	2	E32513	Ig heavy chain pre	
2	2	593.5	79.2	139	1	MHMS18	Ig heavy chain pre	
3	3	592.5	78.3	141	2	JL0076	Ig heavy chain pre	
4	4	579.5	76.6	135	2	A30577	Ig heavy chain pre	
5	5	576	76.1	131	2	A27472	Ig heavy chain pre	
6	6	559	73.8	138	1	HVMS77	Ig heavy chain pre	
7	7	556	73.4	117	1	HVMS02	Ig heavy chain pre	
8	8	555	73.3	136	2	B47159	Ig heavy chain v r	
9	9	554.5	73.2	137	1	G2MS43	Ig heavy chain pre	
10	10	552	72.9	136	2	PL0208	Ig heavy chain pre	
11	11	551.5	72.9	137	2	E29380	Ig heavy chain pre	
12	12	551.5	72.9	137	2	E29380	Ig heavy chain pre	
13	13	546.5	72.2	136	2	JL0077	Ig heavy chain pre	
14	14	543	71.7	117	1	HVMS3	Ig heavy chain pre	
15	15	537	70.9	117	1	HVMS1	Ig heavy chain pre	
16	16	533.5	70.5	120	2	B22769	Ig heavy chain pre	
17	17	533	70.4	140	2	PH1482	Ig heavy chain v r	
18	18	532	70.3	140	1	HVMSG7	Ig heavy chain v r	
19	19	529.5	69.9	139	2	PS0024	Ig heavy chain pre	
20	20	537.5	69.7	120	2	S41394	Ig heavy chain pre	
21	21	527	69.6	117	1	HVMS23	Ig heavy chain pre	
22	22	525	69.4	117	1	MHMSB4	Ig heavy chain v r	
23	23	524	69.2	138	2	S21810	Ig heavy chain pre	
24	24	523	69.1	116	2	I84704	Ig heavy chain pre	
25	25	520	68.7	140	2	PH1489	Ig heavy chain v r	
26	26	519.5	68.6	116	2	S53751	Ig heavy chain v r	
27	27	519	68.6	117	1	HVMS45	antibody Fab Jel 1	
28	28	518.5	68.5	139	2	A27609	Ig heavy chain pre	
29	29	517.5	68.4	141	2	A39276	Ig heavy chain pre	

A:Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
A:Accession: B90809

Qy 1 MGWSCII:FLVSTATSVHSQVLOQPGAELVKPGTSVKLSCKGYGTYTTSYMHVWKQP 60

nb 1 MGWSC:TW:FLAATATGVHSQVLOQPGAELVKPGASVKLSCKASGYTTSYMHVWKQP 60

Query Match 76.1%; Score 576; DB 2; Length 131;
Best Local Similarity 82.8%; Pred. No. 4.7e-42;
Matches 111; Conservative 4; Mismatches 15; Indels

```
Qy 1 MGWSCIIILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGWSYIILFLVATATDVHSQVLOQPGAEVLKPGASVKLSCKASGYTFTSYMMHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GQGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCARGY 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLDWIGEINPNSGRNTYNEKFKSKATLTVDKSSSTAYMQLSSLTSDSAVYYCASDY 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 DGWDYADYWGQGT 134
| | | | |
Db 121 D-W----FAYWGQGT 130
| | | | |

RESULT 6
HVMST7
Ig heavy chain precursor V region (TEPC 1017) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 30-May-1997
C:Accession: A02033
R:Gilliam, A.C.; Shen, A.; Richards, J.E.; Blattner, F.R.; Mushinski, J.F.; Tucker, P.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4164-4168, 1984
A:Title: Illegitimate recombination generates a class switch from C-mu to C-delta in an
A:Reference number: A02033; MUID:84248078
A:Accession: A02033
A:Molecule type: mRNA
A:Residues: 1-138 <GTL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig heavy chain V region (TEPC 1017) #status predicted <MAT>
F:21-117/Region: V segment
F:34-117/Domain: immunoglobulin homology <IMM>
F:118-123/Region: D segment
F:124-138/Region: J segment

Query Match 73.8%; Score 559; DB 1; Length 138;
Best Local Similarity 75.9%; Pred. No. 1.4e-40;
Matches 107; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

Qy 1 MGWSCIIILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGWSYIILFLVATATDVHSQVLOQPGAEVLKPGASVKLSCKASGHTFTNWIHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GQGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCARG-G 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGEINPDGRSNYNEKFKKATLTVDKSSSTAYMQLSLTPPEFAVYYCARSDG 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 120 YDGWDYADYWGQGTSTVSS 140
| | | | |
Db 121 YYDW---FVYWGQGLVTFS 138
| | | | |

RESULT 7
HVM502
Ig heavy chain precursor V region (102) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
C:Accession: A02032
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
A:Reference number: A90809; MUID:81234548
A:Accession: A02032
A:Molecule type: DNA
A:Residues: 1-117 <BOT>
A:Note: the sequence was determined from the germline gene
A:Note: the germline gene, cloned from a library of strain C57BL/6 DNA, is one of a set
C:Genetics: 1 (NPb antibodies)
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (102) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 556; DB 1; Length 117;
Best Local Similarity 89.7%; Pred. No. 2.1e-40;
Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGWSCIIILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGWSCIIILFLVATATGVHSHVLOQPGAEVLKPGASVKVSKASGYTFTSYMMHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GQGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCA 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGRIHPSDSDTNYNOKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYYCA 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8

B47159
Ig heavy chain V region, anti-carcinoembryonic maId T84.66 antigen monoclonal anti-id
C:Species: Mus musculus (house mouse)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: B47159
R:Gaïda, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A:Title: Molecular characterization of a cloned idiotype cascade containing a networ
A:Reference number: A47159; MUID:93300804
A:Accession: B47159
A>Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-136 <GAI>
A:Experimental source: hybridoma 606.C4
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBI:P:134422)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 555; DB 2; Length 136;
Best Local Similarity 75.7%; Pred. No. 2.9e-40;
Matches 106; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

Qy 1 MGWSCIIILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MGWSYIILFLITATCTVHSQVLOQPGAEVLKPGASVKLSCKASGYTFTTMMNWLKQRP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GQGLEWIGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCARGY 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQGLEWIGRIDPYDSVTHYNOKFRDKATLTVDKSSSTAFMQLSSLTSDSAVYYCTRM DY 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 DGWDYADYWGQGTSTVSS 140
| | | | |

Db 121 GNH----DYWGQGTTLTVSS 136
| | | | |

RESULT 9

G2MS43
Ig heavy chain precursor V region (S43) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: A02038
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A:Reference number: A90809; MUID:81234548
A:Accession: A02038
A:Molecule type: mRNA
A:Residues: 1-137 <BOT>
A:Cross-references: GB:J00539; NID:g195118; PIDN:AAA38172.1; PID:g195119
A:Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies to the

C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <STG>
F; 30-137/Product: Ig heavy chain V region (S43) #status predicted
F; 34-117/Domain: immunoglobulin homology <IMM>
F; 118-122/Region: D segment
F; 123-137/Region: J segment (JH2)

```

Query Match      73.28; Score 554.5; DB 1; Length 137;
Best Local Similarity 74.19; Pred. No. 3.3e-40;
Matches 106; Conservative 9; Mismatches 19; Indels 9; Gaps.
2:

Qy    1  MGWSCIIFLVSTATSVHVSQVLOQPQGAEIVKPGTSVKLSCKGCGYTTFTSYMHMVNORP  60
       |||||::||: :|| ||||||:||||| ||||| ||||| ||||| ||||| |||||
Db    1  MGWSCIMFLAATGYVHVSQVLOQPQGEFVKPGASVKLSCKASGYTTFTSYLMHVNORP  60
       |||||::||: :|| ||||||:||||| ||||| ||||| ||||| ||||| |||||

Qy    61  GGLEWICEIDPSSENNTNYNFKGKAPLTVDISSTAYMQLSSITSEDSAVYYCAR --- 117
       |||||:|||| :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db    61  GRGLEWICRIDPSGGTTYNEHFERSKAPLTIIDKFSSRAYMQLSSITSEDSAVYYCARYL 120
       |||||:|||| :||: :||: :||: :||: :||: :||: :||: :||: :||:

Qy   118  GYGWDYAIIDYGGGTSTVTSS 140
       || |
Db   121  GR Y-----FDYWGQGTTLTVSS 137

```

RESULT 10
PL0208
Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/c)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C:Accession: PL0208
R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reacting with the idiotype of an anti-mouse IgG monoclonal antibody
A:Reference number: PL0207; MUID:90309764
A:Accession: PL0208
A:Molecule type: mRNA
A:Residues: 1-136 <SOU>
A:Experimental source: hybridoma cell E225
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:118-125/Region: complementarity-determining 3
F:118-121/Region: D region
F:122-136/Region: JH region

	Query Match	72.9%; Score 552; DB 2; Length 136;
	Best Local Similarity	73.6%; Pred. No. 5.3e-40;
	Matches 103; (conservative	15; Mismatches 18; Indels 4; Gaps 1
Qy	1 MGWSCIIFLYSTATSVHSOVLQPGLVKPCTSVKLSCKGYCTTSYMHVWKORP	60
	: : : : : : : : : :	
Dd	1 MGWSFIIFLVATASGVTSOVLQPGLVRPGASVKLSCKASYTTNTYMHVWKORP	60
Qy	61 CQGLEWICEIDPSENTNMYOKFKATLTVDISSTAYMQLSSITSEDSAVYYCARGY	120
	: : : : : : : : :	
Dd	61 CQGLEWICNIYPGSDSNDEKFSKALTVDTSSTAYMQLSGLTSEDSAVYYCAR---	117
Qy	121 DGWDYAIHWQGQTSTVTYSS	140
	: : :	
Dd	118 -GLAFYFLHWGGTTLTVSS	136

```

RESULT 11
E29380
Iq heavy*chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C:Accession: E29380

```

J:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
 R. Biol. Chem. 262, 13579-13583, 1987
 A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variab
 A:Reference number: A92612; MUID:88007582
 A:Accession: E29380
 A:Molecule type: mRNA
 A:Residues: 1-137 <CHE>
 A:Cross-references: GB:M17164; GB:J02815; NID:q19541; PID:AAA38295.1; PID:q195412
 C:Superfamily: immunoglobulin v region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	72.98;	Score	551.5;	DB 2;	Length	137;			
Best Local Similarity	77.98;	Pred. No.	5.8e-40;						
Matches	109;	Conservative	8;	Mismatches	20;	Indels	3;	Gaps	
Qy	1	MGWSVILFLVSTATSVHSQVLOQPGAELVKPGTSVKLSCKGCGYTTFSYMMHWVKRP	60						
Db	1	MGWSVILFLVTTATGVHSQVLOQPGAELVKPGTSVKLSCKASGYNTFTSWINWVKLRP	60						
Qy	61	QGGLWEIGEDIPSESNTNYNKFKGKALTVDISSTAYMOLSSLTSDSAVYYCARGY	120						
Db	61	QGGLWIGDIYPGSGITNYNEKFSKALTVDTSSTAYMOLSSLSDSALYYCA-QGY	119						
Qy	121	DGWDYAIIDYGGQGTSTVTSS	140						
		:							
Db	120	GNLMFA--YWGQGTITVTSA	137						

RESULT 12

F29380

Ig heavy chain precursor V region (A003 40/5G7) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: F29380

R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.

J. Biol. Chem. 262, 13579-13583, 1987

A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable region of mouse Ig heavy chain precursor V region

A:Reference number: A92612; MUID:88007582

A:Accession: F29380

A:Molecule type: mRNA

A:Residues: 1-137 <CHE>

A:Cross-references: GB:W17165; GB:J02815; NID:gl95409; PIDN:AAA38294.1; PID:gl95410

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	72.9%	Score	551.5	DB 2;	Length	137;
Best Local Similarity	75.0%;	pred.	No. 5.8e-40;			
Matches	105;	Conservative	12;	Mismatches	20;	Indels . 3; Gaps
Qy	1	MCWSCIILFLVSTATSVHSOVLOQPQGAEIVKPGTSVKLSCKGCGYTTFSYWMHWVKORP	60			
Dd	1	MGWNIIILFLVATATGVHSOVQVOQPQGAEIVKPGTSVKLSCKASGYNTFTTWINWKLRP	60			
Qy	61	GCGLEWIGEIDPSESNTRYNYKFKGKATLTVDISSTAYMQLSSITSDSVAYYICARGGY	120			
Dd	61	GCGLEWIGDIYPGSGSTNYNEKFKSKATLTVDTSSTAYMQLSSLASEDSALYYCARQVG	120			
Qy	121	DGDYDAIDYWGGGTSTVTSSS	140			
Dd	121	ETW---FAYWGGLTVTWSA	137			

RESULT 13
 JL0077
 Ig heavy chain precursor V region (anti-phenylloxazalone, 676) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
 C:Accession: JL0077
 R:Kaartinen, M.; Rocca-Serra, J.; Mäkeläe, O.


```

RESULT 15
HVM561
Ig heavy chain precursor V region (186-1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 23-Aug-1996
C:Accession: D90809; A02036; B02034
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies:
A:Reference number: A90809; MUID:81234548
A:Accession: D90809
A:Molecule type: DNA
A:Residues: 1-117 <BOT>
A>Note: the sequence was determined from the germline gene
A>Note: the 186-1 germline gene, cloned from a library of strain C57BL/6 DNA, belongs
C:Genetics:
A: Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (186-1) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

```

	Query Match	70.9%	Score 537;	DB 1;	Length 117;
	Best Local Similarity	84.6%	Pred. No.	8.3e-39;	
	Matches	99;	Conservative	5;	Mismatches 13; Indels 0; Gaps 0;
Qy	1	MGWSGIILFLVSTATSVHSQVOLQPQAELVKPGTSVKLSCKGCGYTTFTSYMHVWKRP	60		
		: : : : :			
Db	1	MGWSICMLFLAATATGVHSQVOLQPQAELVKPGASVKLSCKACGYTFTSYMHVWKRP	60		
Qy	61	GQGLEWIGEIDPSRNTNNYNKFKGKATLTVDIISSTAYMOLSSLTSDSVAIYYCAR	117		
		:			
Db	61	GRGLEWIGRIDPNSGGTYNKFSKATLTVDTSSTAYMOLHSLTSDSVAIYYCAR	117		

Search completed: April 13, 2001, 15:36:47
Job time: 134 sec

```

RESULT      14
HVM53
Ig heavy chain precursor V region (3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 23-Aug-1996
C:Accession: A02031
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some
A:Reference number: A90809; MUID:81234548
A:Accession: A02031
A:Molecule type: DNA
A:Residues: 1-117 <BOT>
A:Note: the sequence was determined from the germline gene
A:Note: the garmline gene, cloned from a library of strain C57BL/6 DNA, is one of a set
1 (NPb antibodies)
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMW>

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Query Match	71.7%	Score 543;	DB 1;	Length 117;
Best Local Similarity	88.0%	Pred. NO. 2.6e-39;		
Matches 103; Conservative		5; Mismatches 9;	Indels 0;	Gaps 0;

[illegible]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:40:18 ; Search time 21.32 Seconds
(without alignments)
224.942 Million cell updates/sec

Title: US-08-700-737-15

Perfect score: 757

Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGWDYADYWGQTSVTYSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	599.5	79.2	139	1 HV07_MOUSE	P01751 mus musculus
2	559	73.8	138	1 HV48_MOUSE	P03980 mus musculus
3	556	73.4	117	1 HV06_MOUSE	P01750 mus musculus
4	554.5	73.2	117	1 HV11_MOUSE	P01755 mus musculus
5	543	71.7	117	1 HV03_MOUSE	P01749 mus musculus
6	537	70.9	117	1 HV09_MOUSE	P01753 mus musculus
7	532	70.3	140	1 HV02_MOUSE	P01746 mus musculus
8	527	69.6	117	1 HV04_MOUSE	P01748 mus musculus
9	525	69.4	117	1 HV09_MOUSE	P06328 mus musculus
10	519	68.6	117	1 HV10_MOUSE	P01754 mus musculus
11	497	65.7	136	1 HV15_MOUSE	P01759 mus musculus
12	479.5	63.3	120	1 HV50_MOUSE	P06329 mus musculus
13	468	61.8	120	1 HV03_MOUSE	P01747 mus musculus
14	447	59.0	117	1 HV12_MOUSE	P01756 mus musculus
15	447	59.0	121	1 HV01_MOUSE	P01745 mus musculus
16	445	58.9	117	1 HV52_MOUSE	P06327 mus musculus
17	445	58.8	117	1 HV13_MOUSE	P01757 mus musculus
18	444	58.7	117	1 HV14_MOUSE	P01758 mus musculus
19	441.5	58.3	118	1 HV51_MOUSE	P06330 mus musculus
20	422.5	55.8	147	1 HV1C_HUMAN	P01744 homo sapien
21	412	54.4	117	1 HV1G_HUMAN	P23083 homo sapien
22	398	52.6	117	1 HV1B_HUMAN	P01743 homo sapien
23	348	46.0	117	1 HV02_MOUSE	P01812 mus musculus
24	347.5	45.9	114	1 HV00_MOUSE	P01741 mus musculus
25	341.5	45.1	119	1 HV38_MOUSE	P01808 mus musculus
26	341.5	45.1	136	1 HV16_MOUSE	DISULFID 41
27	339	44.8	142	1 HV01_RAT	P01783 mus musculus
28	335	44.3	117	1 HV41_MOUSE	P01805 rattus norv
29	333.5	44.1	119	1 HV37_MOUSE	P01811 mus musculus
30	331.5	43.8	146	1 HV21_HUMAN	P01807 mus musculus
31	327	43.2	118	1 HV39_MOUSE	P06331 homo sapien
32	325.5	43.0	119	1 HV40_MOUSE	P01809 mus musculus
33	319	42.1	121	1 HV3J_HUMAN	P01810 mus musculus
					P01771 homo sapien

34 316 41.7 125 1 HV1F_HUMAN P06326 homo sapien
35 312 41.2 117 1 HV1A_HUMAN P01742 homo sapien
36 311.5 41.1 122 1 HV3G_HUMAN P01768 homo sapien
37 308 40.7 115 1 HV32_MOUSE P01801 mus musculus
38 306.5 40.5 126 1 HV3K_HUMAN P01772 homo sapien
39 306 40.4 113 1 HV30_MOUSE P01799 mus musculus
40 305.5 40.4 120 1 HV1H_HUMAN P0421 homo sapien
41 304 40.2 116 1 HV36_MOUSE P01806 mus musculus
42 303.5 40.1 124 1 HV1D_HUMAN P01760 homo sapien
43 302.5 40.0 111 1 HV35_MOUSE P01804 mus musculus
44 301 39.8 113 1 HV27_MOUSE P01796 mus musculus
45 301 39.8 123 1 HV25_MOUSE P01794 mus musculus

ALIGNMENTS

RESULT 1
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; Pubmed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC InterPro; IPR003006; -
CC Pfam; PF00047; ig; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC DOMAIN 20 49 FRAMEWORK 1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
CC DOMAIN 55 68 FRAMEWORK 2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
CC DOMAIN 86 117 FRAMEWORK 3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON_TER 139 139
CC SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 79.2%; Score 599.5; DB 1; Length 139;
Best Local Similarity 80.7%; Pred. No. 2.4e-51;
Matches 113; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

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QY 1 MGWSCIILFLVSTATSVHSGVQLQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
Db 1 MGWSCIIMIPLAATATGATGSHVQVQLQPGAEVLKPGASVKLSCKRSGYTFSTSYNMHWKQRP 60
QY 61 GQGLEWICIDPSESNTNYSNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYCYARG 120
Db 61 GQGLEWICIDPSESNTNYSNOKFKGKATLTVDKPSSTAYMQLSSLTSEDSAVYCYARYD 120
QY 121 DGWDYAILYWGQTSVTSS 140
Db 121 YGSSY-FIYWGQTLTVSS 139
RESULT 2
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980.
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=8424078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR InterPro; IP003006; -.
DR Pfan; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 21 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 1:38 AA; 15576 MW; 748157E4C6907B8E CRC64;
Query Match 73.8%; Score 559; DB 1; Length 138;
Best Local Similarity 75.9%; Pred. No. 2e-47;
Matches 107; Conservative 12; Mismatches 18; Indels 4; Gaps 2;
QY 1 MGWSCIILFLVSTATSVHSGVQLQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
Db 1 MGWSCIIMIPLAATATGATGSHVQVQLQPGAEVLKPGASVKLSCKRSGYTFSTSYNMHWKQRP 60
QY 61 GQGLEWICIDPSESNTNYSNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYCYARG-G 119
Db 61 GQGLEWICIDPSESNTNYSNOKFKGKATLTVDKSSSTAYMQLSSLTPEFAVYCARSDG 120
QY 120 YGWDYAILYWGQTSVTSS 140
Db 121 YIDW---FVWGQTLTVSS 138
RESULT 3
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750.
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02032; HVM502.
DR InterPro; IP003006; -.
DR Pfan; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
Query Match 73.4%; Score 556; DB 1; Length 117;
Best Local Similarity 89.7%; Pred. No. 3.2e-47;
Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MGWSCIILFLVSTATSVHSGVQLQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
Db 1 MGWSCIIMIPLAATATGATGSHVQVQLQPGAEVLKPGASVKLSCKRSGYTFSTSYNMHWKQRP 60
QY 61 GQGLEWICIDPSESNTNYSNOKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYCYA 116
Db 61 GQGLEWIGRIHPSDSDTNYNOKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYCYA 116
RESULT 4
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC EMBL; J00539; AAA38172.1; -.
CC PIR; A02038; G2MS43.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 118 122 FRAMEWORK 3.
FT DOMAIN 123 137 D SEGMENT.
FT DISULFID 41 115 JH2 SEGMENT.
FT NON_TER 137 137 BY SIMILARITY.
SQ SEQUENCE 137 AA; 15200 MW; ADD5861BF44B8EC9 CRC64;

Query Match 73.2%; Score 554.5; DB 1; Length 137;
Best Local Similarity 74.1%; Pred. No. 5.4e-47;
Matches 106; Conservative 9; Mismatches 19; Indels 9; Gaps 2;

QY 1 MCGWSCIILFLVSTATSVHSQVQLQPGAEVLPKPGTSVKLSCKGYGYTFTSYMHVWVQRP 60
DB 1 MCGWSCIILFLAATATGVHSQVQLQPGAEVLPKPGASVKLSCKASGYTFTSYLMHVWVQRP 60
QY 61 GGLGEWIGEIDPSESTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCAR 117
DB 61 GGLGEWIGRIDNSGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYYCARYRL 120
QY 118 GYDCWDYDAIDYWGQGTSTVSS 140
DB 121 GRY-----FDYWGQGTTLTVSS 137

RESULT 5
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR; B02034; HVMS61.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING 2.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 70.9%; Score 537; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 2.2e-45;
Matches -99; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

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CC EMBL; J00536; AAA38605.1; -.
CC PIR; A02031; HVMS3.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match 71.7%; Score 543; DB 1; Length 117;
Best Local Similarity 88.0%; Pred. No. 5.9e-46;
Matches 103; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 MCGWSCIILFLVSTATSVHSQVQLQPGAEVLPKPGTSVKLSCKGYGYTFTSYMHVWVQRP 60
DB 1 MCGWSCIILFLVATATGVHSQVQLQPGAEVLPKPGSSVKLSCKASGYTFTSYMDVWVQRP 60
QY 61 GGLGEWIGEIDPSESTNYNOKFKGKATLTVDISSSTAYMQLSSLTSDSAVYYCAR 117
DB 61 GGLGEWIGNIYPSDSETHYNOKFKDKATLTVDKSSSTAYMQLSSLTSDSAVYYCAR 117

RESULT 6
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC PIR; B02034; HVMS61.
CC InterPro; IPR003006; -.
CC Pfam; PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 70.9%; Score 537; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 2.2e-45;
Matches -99; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MGWSCILFLVSTATSVHSOVQLOQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSCILFLAATATGVSQVQLOQPGAEVLKPGASVKLSCKKASGYTFTSYNMHWKQRP 60
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GQGLEWIGTIDPSESNTNYPKFKGKATLVDTSSSTAYMQLSLTSEDSAVYYCAR 117
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GRGLEWIGTIDPNSGGTKYNEKFKSKATLVDTSSSTAYMQLSLTSEDSAVYYCAR 117
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=C57BL/6;
RX MEDLINE=82153818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
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CC -----
CC EMBL: J00493; AAA38128.1;
DR PIR: A02028; HVMG7.
DR InterPro: IPR003006;
DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
FT SEQUENCE 110 AA; 15514 MW; 2544CBBE31DA5CE8 CRC64;

Query Match 70.3%; Score 532; DB 1; Length 140;
Best Local Similarity 72.1%; Pred. No. 8.4e-45;
Matches 101; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHSOVQLOQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSEFIFLFLSVTAGVHSEVQLOQSGAEVLVRAAGSVKMSCKASGYTFTSYGINWVQRP 60
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GQGLEWIGTIDPSESNTNYPKFKGKATLVDTSSSTAYMQLSLTSEDSAVYYCAR 120
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWISYINPGNGYINYPKFKGKATLVDTSSSTAYMQLSLTSEDSAVYFCARSHY 120
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DGWDYAIYMGQGTSTVSS 140
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 YGGSYDFYMGQGTPLVSS 140
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
HV04_MOUSE STANDARD; PRT; 117 AA.
ID HV04_MOUSE
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC
DR PIR: A02030; HVM23.
DR InterPro: IPR003006;
DR Pfam: PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 69.6%; Score 527; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 2.1e-44;
Matches 98; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHSOVQLOQPGAEVLKPGTGVKLSCKGKGYTFTSYNMHWKQRP 60
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGWSCILFLVAAAANGVHSOVQLOQPGTGVKPGASVKLSCKKASGYTFTSYNMHWKQRP 60
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GQGLEWIGTIDPSESNTNYPKFKGKATLVDTSSSTAYMQLSLTSEDSAVYYCAR 117
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GQGLEWIGNINPGNGTNYNEKFKSVTLTVDKSSSTAYTQLSLTSEDSAVYYCAR 117
      |||||: 11 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
HV49_MOUSE STANDARD; PRT; 117 AA.
ID HV49_MOUSE
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC -----
CC EMBL: M13788; AAA38506.1; -
CC PIR: A02035; HVM5B4.
CC InterPro: IPR003006; -
CC Pfam: PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 59 68 FRAMEWORK 3.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DISULFID 86 117 FRAMEWORK 3.
FT NON_TER 41 115 BY SIMILARITY.
FT SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 69.4%; Score 525; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 3.2e-44;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
Db 1 MGWSCIMFLAATATGVHVSQVLOQPGAEVLKPGASVKLSCKASGYTFTSYMMHWKQRP 60
QY 61 GCGLEWIGIDPSESTNTYNOFKFKATLTVDISSSTAYMOLSSLTSEDSAVYYCAR 117
Db 61 GRGLEWIGNIDPNSGTYNEKFKSKATLTVDKPSSTAYMOLSSLTSEDSAVYYCTR 117

RESULT 10
HV10_MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6780376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
CC EMBL: J00533; AAA38602.1; -
CC PIR: C02034; HVM545.
CC InterPro: IPR003006; -
CC Pfam: PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK 1.
FT SEQUENCE 50 54 COMPLEMENTARITY-DETERMINING 1.

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FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12921 MW; D37DEBA3F543E996 CRC64;

Query Match 68.6%; Score 519; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 1.2e-43;
Matches 97; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
Db 1 MGWSCIMFLAATATGVHVSQVLOQPGAEVLKPGASVKLSCKASGYTFTSYMMHWKQRP 60
QY 61 GCGLEWIGIDPSESTNTYNOFKFKATLTVDISSSTAYMOLSSLTSEDSAVYYCAR 117
Db 61 GRGLEWIGNIDPNSGTYNEKFKSKATLTVDKPSSTAYMOLSSLTSEDSAVYYCAR 117

RESULT 11
HV15_MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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CC -----
CC EMBL: J00494; AAA38130.1; -
CC PIR: A02042; HVM5B1.
CC InterPro: IPR003006; -
CC Pfam: PF00047; Ig; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 65.7%; Score 497; DB 1; Length 136;
Best Local Similarity 68.3%; Pred. No. 2e-41;
Matches 97; Conservative 12; Mismatches 25; Indels 8; Gaps 2;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEVLKPGTSVKLSCKGKGYTFTSYMMHWKQRP 60
Db 1 MGWSCIMFLAATATGVHVSQVLOQPGAEVLKPGASVKLSCKGKGYTFTSYMMHWKQSH 60
QY 61 GCGLEWIGIDPSESTNTYNOFKFKATLTVDISSSTAYMOLSSLTSEDSAVYYCAR--G 118
Db 61 AKSLEWIGISTYNGNTSYNQKFKATMTVDKSSSTVHMLARLTSEDSANLYCARYYG 120

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QY 119 GYDGDYDAIDYWGQTSVTSS 140
DB 121 NY-----FDYWGQGTTLTVSS 136

RESULT 12
HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=8418;519; PubMed=6201362;
RA Dildrop R., Hovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:511-523(1984).
DR PIR: A02037; MHMS15.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
FT SEQUENCE 130 AA; 13311 MW; 914453F426F09834 CRC64;
SQ

Query Match 63.3%; Score 479.5; DB 1; Length 120;
Best Local Similarity 75.2%; Pred. No. 8.4e-40;
Matches 91; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 20 QVLOQPAGELVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGGLEWIGIDPSESNTNY 79
DB 1 QVQLQPGITELVPGASVNLSCASGYTFTSYMMHWIRQPGQGLEWIGINFSNGTNY 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYICARGYDGDYDAIDYWGQTSVTSS 139
DB 61 NEKFKGKATLTVDKSSATYMQLSLTPTSDSAVYICARWDYEG-DRYFDVWGTTVTSS 119
QY 140 S 140
DB 120 S 120

RESULT 13
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FRGM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).

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CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
DR PIR: A02028; HVM5G7.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsenate antibody; Hybridoma.
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13307 MW; FF04B4A167B654AF CRC64;
SQ

Query Match 61.8%; Score 468; DB 1; Length 120;
Best Local Similarity 74.2%; Pred. No. 1.1e-38;
Matches 89; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 21 VLOQPAGELVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGGLEWIGIDPSESNTNY 80
DB 1 VLOQSGAELVRAGSVKMSCKASGYTFTSYGNWKQRPQGGLEWIGINFGNYTKYN 60
QY 81 QKFKGKATLTVDISSSTAYMQLSLTSDSAVYICARGYDGDYDAIDYWGQTSVTSS 140
DB 61 EKFEGKATLTVDKSSSTAYMQLSLTSDSAVYICARSVYIGSYFYDYGQGTTLTVSS 120

RESULT 14
HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MHMS4E.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
SQ

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Query Match 59.0%; Score 447; DB 1; Length 117;
Best Local Similarity 71.1%; Pred. No. 1.1e-36;
Matches 86; Conservative 12; Mismatches 19; Indels 4; Gaps 1;

QY 20 QVLOQPAGELVKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGGLEWIGIDPSESNTNY 79
DB 1 EVQLQSGPGLVLPFGASVKMSCKASGYTFTDYIMKWKQSKSLKSLWIGIDPNNGTST 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSLTSDSAVYICARGYDGDYDAIDYWGQTSVTSS 139
DB 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYICAR-----DYDWYFDVWGAGTTVTSS 116
QY 140 S 140
DB 117 S 117

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RESULT 15
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RL region of immunoglobulin heavy chain MPC11.";
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11
DR InterPro; IPR003006; -.
DR Pfam; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
```

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Query Match 59.08; Score 447; DB 1; Length 121;
Best Local Similarity 69.4%; Pred. No. 1.2e-36;
Matches 84; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

Qy 20 QVQLQQPGAEVLKPKTSVKLSCKGYGTFTSYWMHWKQRPQGLEWIGTIDPSESNTNY 79
: |||| |||||:|||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 1 EAQLQSGAEVLKPKTSVKLSCKAGYFTNYIGWVKRPGHLEWIGDIYPCGGFTNY 60

Qy 80 NQKFKGKATLTVDISSTAYNQLSLSLTSSEDSAVYICARGGYDGDYDAIDYWGQGTSTVTS 139
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 61 NDNLKGRATLTADTSSSTAYIQLSLSLTSSEDSAIYHCARGIYNSSPYFDSWGQGTTLTVS 120

Qy 140 S 140
Db 121 S 121
```

Search completed: April 13, 2001, 15:40:19
Job time: 272 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2001, 15:39:54 ; Search time 56.51 Seconds
(without alignments)
290.375 Million cell updates/sec

Title: US-08-700-737-15
 Perfect score: 757
 Sequence: 1 MGWSCILFLVSTATSVHSQ.....DGWDYATDYWGQGSVTVSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Model	Number of hits	Number of parameters
Model 1	374700	374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : SPTREMBL_15:★

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1:  sp_archea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	473	62.5	117	11	Q9XE9	Q9xe9 mus musculu	
2	464.5	61.4	110	11	Q9JL77	Q9jl77 mus musculu	
3	462.5	61.1	114	11	Q9JL81	Q9jl81 mus musculu	
4	459	60.6	117	11	Q9QXF0	Q9qxf0 mus musculu	
5	458.5	60.6	118	11	Q9Z1C4	Q9z1c4 mus musculu	
6	442.5	58.5	109	11	Q9JL75	Q9jl75 mus musculu	
7	437	57.7	117	11	Q9Z1C6	Q9z1c6 mus musculu	
8	414.5	54.8	124	4	Q9UL92	Q9ul92 homo sapien	
9	414	54.7	119	4	Q9UL94	Q9ul94 homo sapien	
10	412.5	54.5	110	11	Q9JL83	Q9jl83 mus musculu	
11	404	53.4	150	4	Q9Y298	Q9y298 homo sapien	
12	390	51.5	125	4	Q9UL95	Q9ul95 homo sapien	
13	386	51.0	109	11	Q9JL85	Q9jl85 mus musculu	
14	386	51.0	157	4	Q9S978	Q9s978 homo sapien	
15	356.5	47.1	116	4	Q9UL89	Q9ul89 homo sapien	
16	354.5	46.8	298	11	Q9QYF0	Q9qyf0 mus musculu	
17	323	42.7	116	4	Q9UL93	Q9ul93 homo sapien	
18	317	41.9	113	4	Q9UL90	Q9ul90 homo sapien	
19	313.5	41.4	147	4	Q9Y509	Q9y509 homo sapien	

20	301.5	39.8	118	4	Q9UL91	Q9ul91	homo sapien
21	301	39.8	131	4	Q9UL88	Q9ul88	homo sapien
22	300	39.6	121	4	Q9UL71	Q9ul71	homo sapien
23	294.5	38.9	122	4	Q9UL84	Q9ul84	homo sapien
24	291	38.4	119	4	Q9UL73	Q9ul73	homo sapien
25	284.5	37.6	118	4	Q9UL72	Q9ul72	homo sapien
26	284.5	37.6	150.	4	Q9S973	Q9s973	homo sapien
27	278.5	36.8	437	11	Q9RLA4	Q9rla4	mus musculus
28	278	36.7	102	11	Q9JL79	Q9jl79	mus musculus
29	275.5	36.4	124	6	Q9N0W6	Q9n0w6	oryctolagus
30	273.5	36.1	124	6	Q9N0W4	Q9n0w4	oryctolagus
31	265	35.0	95	4	Q9ULB6	Q9ulb6	homo sapien
32	253	33.4	112	4	Q9UGP3	Q9ugp3	homo sapien
33	252	33.3	104	4	Q9UL87	Q9ul87	homo sapien
34	239.5	31.6	122	4	Q9UL75	Q9ul75	homo sapien
35	216	28.5	121	4	Q9UL96	Q9ul96	homo sapien
36	212	28.0	82	4	Q9S729	Q9s729	homo sapien
37	203	26.8	88	4	Q9S737	Q9s737	homo sapien
38	202	26.7	76	4	Q9S742	Q9s742	homo sapien
39	199	26.3	118	4	Q9UL74	Q9ul74	homo sapien
40	196	25.9	77	4	Q9S741	Q9s741	homo sapien
41	193.5	25.6	416	4	Q9NPP6	Q9npp6	homo sapien
42	188.5	24.9	77	4	Q9S726	Q9s726	homo sapien
43	188.5	24.9	81	4	Q9S719	Q9s719	homo sapien
44	187.5	24.8	78	4	Q9S730	Q9s730	homo sapien
45	187	24.7	77	4	Q9S728	Q9s728	homo sapien

ALIGNMENTS

[illegible]

Query Match	62.5%;	Score 473;	DB 11;	Length 117;
Best Local Similarity	75.2%;	Pred. No. 3.2e-41;		
Matches 91;	Conservative 10;	Mismatches 16;	Indels 4;	Gaps 1;
QY	20	QVQLQPGAEIVKPGTISVKLSCKGKGYFTFTSYMMHWVKRPGGGLGWIGEDIPSESNTNY	79	
Db	1	EVQLQSGPELVKPGASVKMSCKASGYFTDYIMKWKQSHGKSLIEWIGDINPNNGCTSY	60	
QY	80	NQKFKGKATLTVDIISSTAYMQLSSTSDSVAVYVCARGGYDGMWDIAIDYWGOGTSVTVS	139	
Db	61	NQKFKGKATLTVDKSSSTAYMQLNSLTSDSVAVYCARDRI----	116	
QY	140	S 140		
Db	117	S 117		

RESULT 2

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Q9JL77          PRELIMINARY;          PRT;          110 AA.
ID Q9JL77;
AC Q9JL77;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (JNV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206029; AAF69327.1; -.
FT NON_TER 1
FT NON_TER 110
FT FT
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 61.4%; Score 464.5; DB 11; Length 110;
Best Local Similarity 79.3%; Pred. No. 2.2e-40;
Matches 88; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

Qy 30 LVKPGTSTVKLSCKGYGYFTTSYWMHWVKRPGQGLEWIGEIDPSESNTNYNQKFKGKATL 89
Db 3 LVKPGASVKLSCKASGYFTTSWMHWAKRPGQGLEWIGIEHPNSGHTNNEKFKGKATL 62
Qy 90 TVDISSTAYMQLSSLTSEDSAVYICARGGYDGDWDYDAIDYWGQGTSTVTSV 140
Db 63 TVDTSSSTAYVDSLSTSEDSAVYICAR---QRNRYAMDYWGQGTSTVTSV 110

RESULT 3
Q9JL81          PRELIMINARY;          PRT;          114 AA.
ID Q9JL81
AC Q9JL81;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (JNV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206025; AAF69323.1; -.
FT NON_TER 1
FT NON_TER 114
FT FT
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match 61.1%; Score 462.5; DB 11; Length 114;
Best Local Similarity 77.9%; Pred. No. 3.7e-40;
Matches 88; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

Qy 29 ELVKPGTSVKLSCKGYGYFTTSYWMHWVKRPGQGLEWIGEIDPSESNTNYNQKFKGKAT 88
Db 2 QLVRFGLSVKLSCKASGYFTTSYWMHWVKRPGQGLEWIGMIDPDSPTRLNOKFKDKAT 61

Qy 89 LTVDISSTAYMQLSSLTSEDSAVYICARGGYDGDWD-YAIDYWGQGTSTVTSV 140
Db 62 LTVDKRSISSTAYMQLSSPTSEDSAVYICARNSYGLSYFDYWGQGTTLTVTSV 114

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RESULT 4
ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademackers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBSJ databases.
RE EMBL; AJ25171; CAB65236.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 117
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 60.6%; Score 459; DB 11; Length 117;
Best Local Similarity 72.7%; Pred. No. 8.7e-40;
Matches 88; Conservative 11; Mismatches 18; Indels 4; Gaps

Qy 20 QVQLQPGAEIVKPTSVKLSCKGKGYFTFSYWMHVKQPGGGLWIGIEDPSESNTNY 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPELVKPGASVKSCRASGYFTFDYTKWKVQSHGSLWIGIDINPNGTSY 60
Qy 80 NQKFKGKATLTVDISSTAYMQLSSTSEDSAVYYCARGYDQWDAIDYWGOGTSVTVTS 139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKGKATLTVDKSSSTAYMQLNLSSTSEDSAVYYCARGDQWDAIDYWGOGTTLTVTS 116
Qy 140 S 140
I
Db 117 S 117

RESULT 5
Q9Z1C4 PRELIMINARY; PRT; 118 AA.
ID Q9Z1C4
AC Q9Z1C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.
RA "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U78801; AAD00293.1; -
DR INTERPRO; IPR003006; -
DR PFAM; PF00047; ig; 1.
FT NON_TER 1
FT NON_TER 118
FT SEQUENCE 118 AA; 13036 MW; 90E5EC559D31EC4FC CRC64;
SO SEQUENCE

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Query Match 60.68; Score 458.5; DB 11; Length 118;

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Best Local Similarity 71.8%; Pred. No. 9.8e-40;
Matches 89; Conservative 8; Mismatches 18; Indels 9; Gaps 2;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNY 79
DB 1 QVQVQSGAEALPQWASVKLSCKASGYFTSYMMHWKQRPQGLEWIGAIYPGCDTSTY 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYICAR--GGYDGDWDYVIDYWGQGTSTV 136
DB 61 TQKFRGKATLTADKSSSTAYMQLSSLTSEDSSAVYICARTVGGY-----FDYWGQGTTL 114
QY 137 TVSS 140
DB 115 TVSS 118

RESULT 6
Q9JL75 PRELIMINARY; PRT; 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
FR EMBL; AF206031; AAF69329.1; -.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FT65E441BBF936A6 CRC64;

Query Match 58.5%; Score 442.5; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 3.9e-38;
Matches 86; Conservative 8; Mismatches 14; Indels 5; Gaps 2;

QY 29 ELVKGPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTYNNQKFKGKAT 88
DB 1 ELVKGPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGYINPYNDGTKYNEKEFGKAT 60
QY 89 LTVDISSSTAYMQLSSLTSEDSSAVYICAR--GGYDGDWDYVIDYWGQGTSTVSS 140
DB 61 LTSDKSSSTAYMQLSSLTSEDSSAVYICARDGNYRGF----DYWGQGTTLTVSS 109

RESULT 7
Q9Z1C6 PRELIMINARY; PRT; 117 AA.
AC Q9Z1C6;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IgG2/G4 constant regions block human leukocyte binding to porcine
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endothelial cells.";
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78799; AAD00291.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig: 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 57.7%; Score 437; DB 11; Length 117;
Best Local Similarity 70.2%; Pred. No. 1.6e-37;
Matches 85; Conservative 8; Mismatches 24; Indels 4; Gaps 2;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNY 79
DB 1 QVLOQSGPQLVRPGTSVKLSCKASGYFTSYMMHWKQRPQDLEWIGMIDPSDEVL 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYICARGYDGDWDYVIDYWGQGTSTVTS 139
DB 61 NORLKDRAKLTVDKSSNTAYMQLSSLTSEDSSAVYICTRGEV-SW---PAYWGQGTTLTVTS 116
QY 140 S 140
DB 117 A 117

RESULT 8
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; Ig: 1.
FT NON_TER 1
FT NON_TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 54.8%; Score 414.5; DB 4; Length 124;
Best Local Similarity 64.5%; Pred. No. 3.4e-35;
Matches 80; Conservative 17; Mismatches 24; Indels 3; Gaps 1;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYFTSYMMHWKQRPQGLEWIGEIDPSESNTNY 79
DB 1 EVQLVESCAEVKKPGASVKVSKASGYFTSSYYMMHWKQRPQGLEWIGMIDPSDEVL 60
QY 80 NQKFKGKATLTVDISSSTAYMQLSSLTSEDSSAVYICARGYDGDWDY---IDYWGQGTSTV 136
DB 61 AQKFGQRYTMTDRTSTVYMELSLRSDETSVAVYICARGLYVVVPAFSAFQYWGQGTTLV 120
QY 137 TVSS 140
DB 121 TVSS 124

RESULT 9
```

Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56256.1; -;
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; ig; 1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 54.7%; Score 414; DB 4; Length 119;
Best Local Similarity 65.6%; Pred. No. 3.7e-35;
Matches 80; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 20 QVQLQAPGKGLTVDISSTAYMQLSLTSVDSAVYFCAR---SNVDVRFAYWGQGLTVTVSA 110
Db 1 EVQLVESGGGVQPGASVKSCRASGFTFTGYYMHVVRQAPGQGLEWMGWINPNSWTNY 60
QY 80 NQKPKKGLTVDISSTAYMQLSLTSVDSAVYFCARGYDGDG---WDYADYWGQGLTVTV 138
Db 61 AQRFGKGLTVDISSTAYMQLSLTSVDSAVYFCARGYDGDG---WDYADYWGQGLTVTV 117

QY 139 SS 140
Db 118 SS 119

Query Match 54.7%; Score 414; DB 4; Length 119;
Best Local Similarity 65.6%; Pred. No. 3.7e-35;
Matches 80; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 20 QVQLQAPGKGLTVDISSTAYMQLSLTSVDSAVYFCAR---SNVDVRFAYWGQGLTVTVSA 110
Db 1 EVQLVESGGGVQPGASVKSCRASGFTFTGYYMHVVRQAPGQGLEWMGWINPNSWTNY 60
QY 80 NQKPKKGLTVDISSTAYMQLSLTSVDSAVYFCARGYDGDG---WDYADYWGQGLTVTV 138
Db 61 AQRFGKGLTVDISSTAYMQLSLTSVDSAVYFCARGYDGDG---WDYADYWGQGLTVTV 117

QY 139 SS 140
Db 118 SS 119

Query Match 54.7%; Score 414; DB 4; Length 119;
Best Local Similarity 65.6%; Pred. No. 3.7e-35;
Matches 80; Conservative 14; Mismatches 24; Indels 4; Gaps 2;

QY 29 ELVKPGTSLVKLSCKGYGTYFTSYWVHWVQKPGQGLEWIGEDPSSTNTYNGKFKGKAT 88
Db 2 ELVKPGASVKISCKASGYTFSNMNMVVKLRPGQGLEWIGRIYPGDGLAYNGKFKGKAT 61

QY 89 LTVDISSTAYMQLSLTSVDSAVYFCARGYDGDG---SNVDVRFAYWGQGLTVTVSA 140
Db 62 LTVDISSTAYMQLSLTSVDSAVYFCAR---SNVDVRFAYWGQGLTVTVSA 110

RESULT 11
Q9Y298 PRELIMINARY; PRT; 150 AA.
ID Q9Y298;
AC Q9Y298;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -;
DR INTERPRO; IPR003006; -;
DR PFAM; PF00047; ig; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 53.4%; Score 404; DB 4; Length 150;
Best Local Similarity 56.4%; Pred. No. 5.2e-34;
Matches 79; Conservative 17; Mismatches 40; Indels 4; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHVSQVQLQPGAEVLKPGTSLVKLSCKGYGTYFTSYWVHWVQK 60
Db 1 MDWTIRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKSVKSGYTLTELPVHWVQAP 60

QY 61 GQGLEWIGEDPSSTNTYNGKFKGKATLTVDISSTAYMQLSLTSVDSAVYFCARGY 120
Db 61 GQGLEWIGEDPSSTNTYNGKFKGKATLTVDISSTAYMQLSLTSVDSAVYFCARGY 120

QY 121 DGWDYADYWGQGLTVTVSS 140
Db 121 D-----AFDINGQGTMTVTVSS 136

RESULT 12
Q9UL95 PRELIMINARY; PRT; 125 AA.
ID Q9UL95;
AC Q9UL95;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

Query Match 54.5%; Score 412.5; DB 11; Length 110;
Best Local Similarity 70.5%; Pred. No. 4.7e-35;
Matches 79; Conservative 8; Mismatches 22; Indels 3; Gaps 1;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:35:39 ; Search time 57.59 seconds
(without alignments)
138.963 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHQS.....DGWDYAIYWGQTSVTYSS 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
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7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.*
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19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	757	100.0	140	19 W53815	Murine Act-1 heavy
2	730	96.4	137	19 W53818	Protein sequence O
3	713	94.2	144	19 W53816	Consensus protein
4	632	83.5	180	19 W53813	Heavy chain of a h
5	615	81.2	464	19 W83041	Anti-Fas MAB HFE7A
6	615	81.2	464	21 B14747	Mouse anti-Fas ant
7	615	81.2	464	21 W90897	Murine anti-Fas an
8	597	78.9	464	16 R76088	MAB 55.1 heavy cha
9	594.5	78.5	443	18 W24025	Single chain antig
10	589	77.8	140	13 R27049	VH425 antibody clo
11	586	77.4	136	8 P70624	Sequence encoded b

12	586	77.4	136	18 W10584	Anti-hepatitis B h
13	586	77.4	136	18 W16340	Mouse-human chimae
14	586	77.4	136	18 W10239	Chimeric anti-hepa
15	586	77.4	136	19 W47510	Human anti-hepatit
16	586	77.4	136	19 W41054	Human anti-hepatit
17	586	77.4	136	19 W47517	Human anti-hepatit
18	586	77.4	136	20 W89535	Chimeric anti-hepa
19	583	77.0	143	16 R84554	MAB SCH94.03 heavy
20	567	74.9	470	21 W90933	Humanised anti-Fas
21	565	74.6	470	21 W90934	Humanised anti-Fas
22	564	74.5	470	19 W83037	Anti-Fas humanised
23	564	74.5	470	21 B14779	Humanised anti-Fas
24	564	74.5	470	21 W90929	Humanised HFE7A de
25	564	74.5	470	21 W90935	Humanised anti-Fas
26	556	73.4	145	19 W83038	Anti-Fas humanised
27	556	73.4	145	21 B14775	Fragment of humani
28	556	73.4	145	21 W90925	Humanised anti-Fas
29	556	73.4	470	19 W83036	Anti-Fas humanised
30	556	73.4	470	21 B14776	Humanised anti-Fas
31	556	73.4	470	21 W90926	Humanised HFE7A de
32	551.5	72.9	143	12 R12233	Humanised HFE7A de
33	551.5	72.9	144	12 R12355	Mouse MAB 2E12 H c
34	549	72.5	138	19 W50218	Heavy chain variab
35	549	72.5	470	21 B08026	Amino acid sequenc
36	548.5	72.5	137	19 W44177	A dimeric anti-CD2
37	545	72.0	140	15 R55215	Monoclonal antibod
38	545	72.0	470	21 W90936	Murine variable re
39	544.5	71.9	139	13 R29009	Humanised HFE7A de
40	543	71.7	140	18 W06213	p64-h2 protein pro
41	543	71.7	140	20 W85061	MAB Co-1 heavy cha
42	538	71.1	119	18 W07436	Mouse Co-1 heavy c
43	537	70.9	140	11 R09425	Anti-DNA antibody
44	536.5	70.9	465	16 R66758	Co-1 Heavy Chain v
45	536	70.8	119	16 R79863	Anti-tobacco mosai
					Anti-EGFR antibody

ALIGNMENTS

RESULT 1	
W53815	ID W53815 standard; Protein; 140 AA.
XX	XX W53815;
AC	AC
XX	XX
DT	14-JUL-1998 (first entry)
XX	XX Murine Act-1 heavy chain variable region.
DE	DE
XX	XX Mouse; Act-1 antibody; human alpha4-beta7 integrin;
KW	KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
KW	KW humanised antibody; murine antigen binding region; inhibition;
KW	KW leukocyte infiltration of tissue; treatment; inflammatory disease;
KW	KW inflammatory bowel disease.
XX	XX Mus. sp.
OS	OS
XX	XX
PH	PH Key Location/Qualifiers
FT	FT Peptide 1..19
FT	FT /note= "signal peptide"
FT	FT Protein 20..140
FT	FT /note= "mature protein"
XX	XX W09806248-A2.
PN	PN
XX	XX
PD	PD 19-FEB-1998.
XX	XX
XX	XX
PF	PF 06-AUG-1997; 97W0-0513884.
XX	XX
PR	PR 15-AUG-1996; 96US-0700737.
XX	XX
PA	PA (LEUK-) LEUKOSITE INC.
XX	XX

XX Bendiq MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
PI

FT Misc-difference 7 /note= "not specified, encoded by RTC"
 FT /note= "encoded by ATY"
 FT Misc-difference 8 /note= "not specified, encoded by YTC"
 FT Peptide 1..19 /note= "signal peptide"
 FT Protein 20..144 /note= "mature protein"
 FT Region 20..49 /note= "framework region 1"
 FT Region 50..54 /note= "CDR1"
 FT Region 55..68 /note= "framework region 2"
 FT Region 69..85 /note= "CDR2"
 FT Region 86..117 /note= "framework region 3"
 FT Region 118..130 /note= "CDR3"
 FT Region 131..141 /note= "framework region 4"
 FT XX
 PN WO9806248-A2.
 XX 19-FEB-1998.
 XX 06-AUG-1997; 97WO-US13884.
 XX 15-AUG-1996; 96US-0700737.
 XX (LEUK-) LEUKOSITE INC.
 XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX WPI; 1998-159172/14.
 DR N-PSDB; V20085.
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX Example 1; Fig 1; 145pp; English.
 XX The present sequence represents the consensus amino acid sequence
 CC comprising the variable region of murine Act-1 antibody determined from
 CC several independent mouse heavy chain variable region clones. Act-1 is
 CC active against human alpha4-beta7 integrin. Muscosal adressin cell
 CC adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin.
 CC The Act-1 antibody interferes with alpha4-beta7 integrin binding to
 CC MadCAM-1, which is present of high endothelial venules in mucosal
 CC lymph nodes. Variable regions were amplified from DNA encoding Act-1
 CC using degenerate PCR primers V20079-82. The degeneracy of the PCR primers
 CC produced several different sequences, of which the present sequence is a
 CC consensus sequence. The present sequence was used to construct
 CC chimeric, humanised Act-1 antibodies, which contain murine antigen
 CC binding regions. The humanised immunoglobulin can be used to inhibit
 CC the interaction of cells bearing alpha4-beta7 with cells bearing a
 CC ligand for alpha4-beta7. It can be used for inhibiting leukocyte
 CC infiltration of tissues, e.g. for treating inflammatory diseases such
 CC as inflammatory bowel disease. The immunoglobulin can also be used for
 CC detection, isolation and diagnosis.
 XX Sequence 144 AA;
 Query Match 94.2%; Score 713; DB 19; Length 144;
 Best Local Similarity 99.3%; Pred. No. 1e-51;
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 ILFLVSTATSVHSGVQLQPGAEIVKPGSVKLSCKGYGYTFTSYMMHWVKRPGQGLEW 66

Db 7 ILFLVSTATSVHSGVQLQPGAEIVKPGSVKLSCKGYGYTFTSYMMHWVKRPGQGLEW 66
 QY 67 IGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGYDGMWYA 126
 Db 67 IGEIDPSESNTNYNOKFKGKATLTVDISSSTAYMQLSLTSEDSAVYYCARGGYDGMWYA 126
 QY 127 IDYWGQGTSTVTVSS 140
 Db 127 IDYWGQGTSTVTVSS 140
 RESULT 4
 W53813
 ID W53813 standard; Protein; 180 AA.
 XX W53813;
 XX 14-JUL-1998 (first entry)
 XX Heavy chain of a humanised murine Act-1 antibody.
 KW Mouse; Act-1 antibody; human alpha4-beta7 integrin;
 KW Muscosal adressin cell adhesion molecule-1; MadCAM-1;
 KW Humanised antibody; murine antigen binding region; Inhibition;
 KW leukocyte infiltration of tissue; treatment; inflammatory disease;
 KW inflammatory bowel disease.
 XX Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..19 /note= "signal peptide"
 FT Protein 20..180 /note= "mature protein"
 FT XX
 PN WO9806248-A2.
 XX 19-FEB-1998.
 XX 06-AUG-1997; 97WO-US13884.
 XX 15-AUG-1996; 96US-0700737.
 XX (LEUK-) LEUKOSITE INC.
 XX Bendig MM, Jones ST, Newman W, Ponath PD, Ringler DJ;
 PI Saldanha J;
 XX WPI; 1998-159172/14.
 DR N-PSDB; V20076.
 XX Humanised immunoglobulin reactive with alpha-4-beta-7 integrin -
 PT used for treating inflammatory disease, pancreatitis, diabetes,
 PT asthma, graft versus host disease and sarcoidosis
 XX Claim 20; Fig 11; 145pp; English.
 XX The present sequence represents the heavy chain of humanised murine
 CC antibody Act-1. Act-1 is active against human alpha4-beta7 integrin.
 CC Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of
 CC this particular integrin. The Act-1 antibody interferes with alpha4-beta7
 CC integrin binding to MadCAM-1, which is present of high endothelial
 CC venules in mucosal lymph nodes. The humanised immunoglobulin can be
 CC used to inhibit the interaction of cells bearing alpha4-beta7 with
 CC cells bearing a ligand for alpha4-beta7. It can be used for inhibiting
 CC leukocyte infiltration of tissues, e.g. for treating inflammatory
 CC diseases such as inflammatory bowel disease. The immunoglobulin can
 CC also be used for detection, isolation and diagnosis.
 XX Sequence 180 AA;

```

Query Match      83.5%; Score 632; DB 19; Length 180;
Best Local Similarity 85.9%; Pred. No. 5.8e-45;
Matches 116; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFLVSTATSVHVSQVLOQPGAEILVKPGTSTVKLSCKGYGTYFTSYNMHWKQRPQGGLE 65
DB 6 VILFLVSTATSVHVSQVLOQPGAEILVKPGTSTVKLSCKGYGTYFTSYNMHWKQRPQGGLE 65
QY 66 WIGEIDP:ESNTNYNQKFKGATFLVDISSSTAYMOLSLTSEDSAVYYCARGGYDGDWY 125
DB 66 WIGEIDP:ESNTNYNQKFKGATFLVDISSSTAYMOLSLTSEDSAVYYCARGGYDGDWY 125
QY 126 AIDYWGQ:TSVTSS 140
DB 126 AIDYWGQ:TLTVSS 140

RESULT 5
W83041
ID W83041 standard; Protein; 464 AA.
XX
AC W83041;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas Mab HFE7A heavy chain.
XX
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy; complementarity determining region;
KW CDR.
XX
OS Mus musculus
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT Region /label= Mat_protein
FT Region 20..140
FT Region /label= Variable
FT Region 141..464
FT Region /label= Constant
FT Region 50..54
FT Region /label= CDR_H1
FT Region /note= "Claim 9"
FT Region 69..84
FT Region /label= CDR_H2
FT Region /note= "Claim 9"
FT Region 118..128
FT Region /label= CDR_H3
FT Region /note= "Claim 9"
XX
PN AU9859701-A.
XX
PD 08-OCT-1998.
XX
PE 30-MAR-1998; 98AU-0059701.
XX
PR 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX

```

(SANYO) SANKYO CO LTD.

Akio S. Hideyuki H. Hiroko Y. Jun O. Kimihisa I;
Masahiko O. Nobufusa S. Shin Y. Tohru T;
WPI: 1998-543440/47.
N-PSDB; V71029.

New antibodies and proteins bind conserved epitope of Fas antigen -
used to evaluate drugs in animal models and to treat Fas-associated
diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
myocarditis, hepatitis and AIDS

Reference Example 4; Page 187-188; 292pp; English.

This is the amino acid of the heavy chain of murine anti-human Fas
monoclonal antibody HFE7A. cDNA (see V70129) encoding the heavy
chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
RNA by RT-PCR (see V70125-26). The invention provides humanised
HFE7A antibodies (see W83031-37) produced by CDR grafting. These
antibodies are capable of inducing apoptosis in abnormal cells
expressing Fas, and of inhibiting Fas-induced apoptosis in normal
cells. They are used to evaluate, in animal models, treatments of
diseases that involve Fas/Fas ligand interactions, and also to treat
such diseases, including autoimmune disease (e.g. systemic lupus
erythematosus, Hashimoto's disease, graft versus host disease,
Sjogren syndrome, pernicious anaemia, Crohn's disease, rheumatoid
scleroderma, Goodpasture syndrome, Crohn's disease, myasthenia
arthritis, autoimmune haemolytic anaemia, sterility, thrombopenia
purpura, multiple sclerosis, Basedow's disease, thrombopenia purpura
and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
anaemia, hepatitis, AIDS and transplant rejection (all claimed).

Sequence 464 AA:

```

Query Match      81.2%; Score 615; DB 19; Length 464;
Best Local Similarity 84.3%; Pred. No. 3.8e-43;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCILFLVSTATSVHVSQVLOQPGAEILVKPGTSTVKLSCKGYGTYFTSYNMHWKQRP 60
DB 1 MGWSCILFLVSTATSVHVSQVLOQPGAEILVKPGTSTVKLSCKGYGTYFTSYNMHWKQRP 60
QY 61 GQGLEWIGEIDPSESTNTNQNPKFKGATFLVDISSSTAYMOLSLTSEDSAVYYCARGGY 120
DB 61 GQGLEWIGEIDPSESTNTNQNPKFKGATFLVDISSSTAYMOLSLTSEDSAVYYCARGGY 120
QY 121 DGWDY AIDYWGQ:TSVTSS 140
DB 121 YSNWYFDWGWG:TLTVSS 140

RESULT 6
B14747
ID B14747 standard; Protein; 464 AA.
XX
AC B14747;
XX
DT 24-NOV-2000 (first entry)
XX
DE Mouse anti-Fas antibody HFE7A heavy chain.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; complementarity determining region; CDR; human Fas;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Mus musculus.
XX

```


RESULT 8
R76088
ID R76088 standard; Protein: 464 AA.
XX
AC R76088;
XX
DT 21-NOV-1995 (first entry)
XX
DE MAb 55.1 heavy chain.
XX
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT 20..464
FT /label= Mat_protein
FT /note= "claim 3, page 97-98"
XX
PN W09515382-A.
XX
PD 08-JUN-1995.
XX
PF 29-NOV-1994; 94WO-GB02610.
XX
PR 03-JUN-1994; 94GB-0011089.
PR 03-DEC-1993; 93GB-0024819.
XX
PA (ZENE) ZENE/A LTD.
XX
PI Blakey DC, Root C, Copley CG, Hall SM, Paterson DS;
PI Rose MS, Wr. ght AF;
XX
XX WPI; 1995-21:262/28.
DR N-PSDB; Q94017.
XX
PT Antigen binding structures containing CDRs recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the
PT diagnosis and therapy of cancer
XX
PS Disclosure; Fig.15; 121pp; English.
XX
CC MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
CC antigen CA55.1. cDNAs for the heavy (Q94037) and light (Q94036)
CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or
CC V-min humanized 55.1 constructs have been expressed in myeloma
CC cells and E. coli.
XX
SQ Sequence 454 AA;

Query Match 78.9%; Score 597; DB 16; Length 464;
Best Local Similarity 80.0%; Pred. No. 1.1e-41;
Matches 112; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGNSCIIFLVSTATSVHSQVQLQQGAEIVKPGTSLVLSCKGSGYFTSYNMHWKQRP 60
DB 1 mgwsyilflvatgtdvhsqvlqqpaaelvkgasvqlsckasgyftgywhwvkqr 60
QY 61 GQGLEWTJEDIPSESNYNNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYICARGY 120
DB 61 gqglewtfjevpnsgrsdynekfnkatltvdkssstaymqlssltsedsavyyicar 120
QY 121 DGWDYAIQYWGQGTSTVTVSS 140

Db 121 ygddamywgqgtstvtvss 140

RESULT 9
W24025
ID W24025 standard; Protein: 443 AA.
XX
AC W24025;
XX
DT 04-MAR-1998 (first entry)
XX
DE Single chain antigen hybrid receptor.
XX
KW Hybrid receptor; single chain antigen; gene therapy; diagnosis;
KW signal conduction; receptor; control region.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= leader_peptide
FT 20..444
FT /note= "single chain antigen hybrid receptor"
FT 20..139
FT /label= VH_B_1-8
FT /note= "variable heavy chain region of B1-8 antibody"
FT 140..154
FT /label= (Gly_Ser)3
FT /note= "linker region"
FT 155..264
FT /label= VL_B_1-8
FT /note= "variable light chain region of B1-8 antibody"
FT 265..309
FT /label= CD_8-alpha_hinge
FT 310..330
FT /label= transmembrane_domain
FT 331..444
FT /label= cytoplasmic_domain
XX
PN W09720938-A2.
XX
PD 12-JUN-1997.
XX
PF 03-DEC-1996; 96WO-DE02334.
XX
PR 05-DEC-1995; 95DE-4045351.
XX
PA (UYPR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
XX
PI Kulmburg P, Mertelsmann R, Rosenthal F;
XX
DR WPI; 1997-319784/29.
DR N-PSDB; T77137.
XX
PT Cells with hybrid receptor having extracellular and intracellular
PT regions of different origins - useful in gene therapy and diagnosis
PT of tumours
XX
PS Example 3; Fig 4; 46pp; German.
XX
CC This sequence represents a novel single chain antigen hybrid receptor
CC (HR) and contains an extracellular domain specific for the hapten
CC 4-hydroxy-3-iodo-3-nitrophenyl acetate (NIP) coupled to the CD8-alpha
CC region and the transmembrane and signal-conducting intracellular parts
CC of the CD3-zeta molecule. Such hybrid receptors comprise a receptor part
CC localised on the outside of the cell and specific to a particular signal
CC molecule and a receptor part originating from another receptor, localised
CC on the inside of the cell and capable of setting off a signal inside the
CC cell. The cell should also contain at least one other gene construct with
CC a control region which can interact with the signal sent out by the
CC hybrid receptor and thereby control expression of a transgene bound to
CC this control region. Such cells are useful in gene therapy or for

XX SQ Sequence 1:6 AA;

Query Match 77.4%; Score 586; DB 8; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.6e-41;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIIILFLVSTATSVHSGVQLQOPGAELVKPGTSVKLSCKGYGTYFTSYWMHWKQRP 60
DB 1 mgwsyililflvatardvhsqvlqqpgaelvkpgasvkscasgytftsywmhwkqrp 60

QY 61 GQGLEWIGETIDPSESNTNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVVYCARGY 120
DB 61 ggglwdwi:geinpsngrtnyefkfskatltvdkssstaymqilssltseavsavycasydy 120

QY 121 DGWDYAIIDYWGQTSVTSS 140
DB 121 d-w---faywgggtlvtss 136

RESULT 12
W10584
ID W10584 standard; Protein: 136 AA.
AC W10584;
XX XX
DT 21-OCT-1997 (first entry)
XX XX
DE Anti-hepatitis B heavy chain variable region.

XX Immunoglobulin G; IgG; heavy chain; recombinant production;
KW antibody; passive immunisation; serum sickness; anaphylactic shock;
KW Immunoassay; imaging; reagent; complement mediated lysis;
KW therapy; hepatitis B virus; variable region; HBV.
XX XX
OS Mus spp.
XX XX
PN US5595898-A.
XX XX
PD 21-JAN-1997.
XX XX
PF 01-NOV-1985; 85US-0793980.
XX XX
PR 29-MAR-1990; 90US-0501092.
PR 01-NOV-1985; 85US-0793980.
PR 27-OCT-1986; 86WO-US02269.
PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0987555.
PR 18-AUG-1994; 94US-0299085.
XX XX
PA (XOMA) XOMA CORP.

XX Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
XX WPI: 1997-107579/10.
DR N-PSDB: T36303, T36304.
XX XX
XX Nucleic acid encoding immunoglobulin fragment - comprising
PT di:clonronic transcription unit with pectate lyase signal sequences
PT di:clonronic transcription unit with pectate lyase signal sequences
XX XX
XX Example; Fig 12B; 95pp; English.

XX The cDNA sequence encoding present anti-hepatitis B heavy chain
CC variable sequence, was used in the preparation of a novel
CC polynucleotide molecule encoding an Ig fragment. The DNA
CC molecule comprises 2 DNA sequences encoding 2 pectate lyase
CC secretion signal sequences respectively linked to a DNA sequence
CC encoding an Ig Fd molecule or Ig light chain, operably linked to a
CC single prokaryotic promoter so as to form a dicistronic
XX transcription unit, provided that the Ig fragment can bind an

CC antigen and is produced and secreted by an E. coli host cell when
CC the nucleic acid molecule is expressed in the host cell.
CC The polynucleotide molecule is used for the production of
CC recombinant antibodies, which can be used for passive immunisation
CC without negative immune reactions (e.g. serum sickness and
CC anaphylactic shock), in labelled forms as immunoassay or imaging
CC reagents, in complement mediated lysis and for therapeutic
CC purposes when coupled to a toxin or other therapeutic agent.

XX SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 18; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.6e-41;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIIILFLVSTATSVHSGVQLQOPGAELVKPGTSVKLSCKGYGTYFTSYWMHWKQRP 60
DB 1 mgwsyililflvatardvhsqvlqqpgaelvkpgasvkscasgytftsywmhwkqrp 60

QY 61 GQGLEWIGETIDPSESNTNOKFKGKATLTVDISSTAYMQLSSLTSEDSAVVYCARGY 120
DB 61 ggglwdwi:geinpsngrtnyefkfskatltvdkssstaymqilssltseavsavycasydy 120

QY 121 DGWDYAIIDYWGQTSVTSS 140
DB 121 d-w---faywgggtlvtss 136

RESULT 13
W16340
ID W16340 standard; Protein: 136 AA.
XX AC W16340;
XX XX
DT 04-SEP-1997 (first entry)
XX XX
DE Mouse-human chimaeric anti-hepatitis B heavy chain.

XX Antibody engineering; heavy chain; light chain; chimaeric antibody;
KW passive immunisation; diagnosis; hybridoma; hepatitis B virus;
KW HBSag; PING2006E; PING2012E.
XX XX
OS Chimaeric Mus sp.;
OS Chimaeric Homo sapiens.

XX Key Location/Qualifiers
FH Protein 1..114
FT /label= VH
FT /note= "mouse heavy chain variable region"
FT Peptide 115..117
FT /label= J
FT /note= "human J region"
FT Misc-difference 117
FT /note= "alteration from mouse to human sequence
FT (Ala to Ser) introduced in the chimaeric
FT J region"

XX US5618920-A.
XX PN
XX 08-APR-1997.
XX PD
XX 01-NOV-1985; 85US-0793980.
XX PF
XX 29-MAR-1990; 90US-0501092.
XX PR 01-NOV-1985; 85US-0793980.
XX PR 27-OCT-1986; 86WO-US02269.
XX PR 24-JUL-1987; 87US-0077528.
XX PR 11-JAN-1988; 88US-0142039.
XX PR 17-APR-1992; 92US-0870404.
XX PR 29-APR-1994; 94US-0235225.
XX PA (XOMA) XOMA CORP.


```

XX
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
XX Wall R, Wilcox GL;
XX
DR WPI; 1997-225473/20.
DR N-PSDB; T70857-58.
XX
PT Secretable immunoglobulin heavy and light chain fragments - capable
PT of assembling into chimeric antibodies, useful for e.g. passive
XX immunisation, diagnosis, etc
XX
PS Example 2; Fig 12B; 96pp; English.
XX
CC A chimeric polypeptide (W16340) comprises a mouse anti-HBsAg
CC heavy chain variable region (derived from hybridoma ATCC CRL8017)
CC and a human J region sequence. It is encoded by DNA sequences in
CC plasmids pING2006E (T70857) or pING2012E (T70858). A complete
CC polypeptide, comprising the mouse anti-HBsAg heavy chain
CC variable region and human constant region, has been expressed in
CC bacterial and transfected mouse cell hosts. Gene amplification has
CC allowed prodn. of chimeric heavy chain.
XX
SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 18; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.6e-41;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHVSQVLOQPGAEIVKPGTSTVKLSCKGCGYTTFTSYMMHWKORP 60
DB 1 mgwsyillflvatardvhsqvlqpgaelvkgasvkscasgyttftsymbhwkqr 60
QY 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMOLSLTSEDSAVYYCARGY 120
DB 61 gggldwigeinpsngrtnynekfkskatltvdkssstaymqsltsedsavyyasydy 120
QY 121 DCWDYADYWGQGTSTVTVSS 140
DB 121 d-w---faywgggtlvtvss 136
QY 121 DCWDYADYWGQGTSTVTVSS 140
DB 121 d-w---faywgggtlvtvss 136

RESULT 14
W10239
ID W10239 standard; Protein; 136 AA.
XX
AC W10239;
XX
DT 05-AUG-1997 (first entry)
XX
DE Chimeric anti-hepatitis heavy chain from pING2006E.
XX
KW Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
KW protein production; human; constant region; passive immunisation; toxin;
KW serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm;
KW antibody; Ig; heavy-chain; hepatitis; mouse; chimera.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus musculus.
XX
PN US5576195-A.
XX
PD 19-NOV-1996.
XX
PF 01-NOV-1985; 85US-0793980.
XX
PR 29-MAR-1990; 90US-0501092.
PR 01-NOV-1985; 85US-0793980.
PR 27-OCT-1986; 86WO-US02269.
PR 24-JUL-1987; 87US-0077528.
PR 11-JAN-1988; 88US-0142039.
PR 08-DEC-1992; 92US-0967555.
PR 22-FEB-1993; 93US-0020671.

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PR 09-DEC-1994; 94US-0357234.
XX (XOMA ) XOMA CORP.
XX
PI Better M, Lei S, Robinson RR, Wilcox GL;
XX
DR WPI; 1997-011254/01.
DR N-PSDB; T51039.
XX
PT Improved prodn. of protein in Gram -ve bacteria using signal
PT sequence - from pectate lyase to ensure transport of protein from
PT the cytoplasm, esp. for prodn. of antibodies
XX
PS Example 2; Fig 12B; 86pp; English.
XX
CC This sequence represents a fragment of the human-mouse chimeric
CC anti-hepatitis heavy chain encoded by the gene contained within
CC pING2006E. pING2006E was used in the method of the invention to express
CC the chimeric heavy chain. The method of the invention is for the
CC production of a protein in a Gram-negative bacterium. The method improves
CC on current techniques, by using a vector including DNA encoding the
CC pectate lyase signal sequence (see T51034), attached to the sequence
CC encoding the protein for production. The method is especially used to
CC make immunoglobulins (Ig), particularly those with a human constant
CC region, suitable for passive immunisation (without risk of serum sickness
CC or anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may
CC also be used therapeutically, optionally coupled to toxins, etc.
CC Alternatively the protein to be produced is the sweetener thaumatin. The
CC presence of this signal sequence means that the protein is exported from
CC the cytoplasm and can be recovered from the culture medium or periplasm,
CC in active and correctly folded form. The method allows the class of any
CC antibody to be switched, e.g. most human-human Ig are of M class, easily
CC reduced and aggregated, and these can now be changed to G, A or E
XX classes.
XX
SQ Sequence 136 AA;

Query Match 77.4%; Score 586; DB 18; Length 136;
Best Local Similarity 81.4%; Pred. No. 2.6e-41;
Matches 114; Conservative 5; Mismatches 17; Indels 4; Gaps 2;

QY 1 MGWSCIILFLVSTATSVHVSQVLOQPGAEIVKPGTSTVKLSCKGCGYTTFTSYMMHWKORP 60
DB 1 mgwsyillflvatardvhsqvlqpgaelvkgasvkscasgyttftsymbhwkqr 60
QY 61 GQGLEWIGEIDPSESNTNYNQKFKGKATLTVDISSSTAYMOLSLTSEDSAVYYCARGY 120
DB 61 gggldwigeinpsngrtnynekfkskatltvdkssstaymqsltsedsavyyasydy 120
QY 121 DCWDYADYWGQGTSTVTVSS 140
DB 121 d-w---faywgggtlvtvss 136
QY 121 DCWDYADYWGQGTSTVTVSS 140
DB 121 d-w---faywgggtlvtvss 136

RESULT 15
W47510
ID W47510 standard; Protein; 136 AA.
XX
AC W47510;
XX
DT 05-JUN-1998 (first entry)
XX
DE Human anti-hepatitis antibody heavy chain.
XX
KW Mouse; murine; human anti-hepatitis antibody; heavy chain;
KW immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody L6; human lung carcinoma cell.
XX
OS Homo sapiens.
XX
PN US5698435-A.
XX

```


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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:49 ; Search time 117.03 Seconds
(without alignments)
192.426 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSQ.....DGWDYADYWGQTSVTYSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1009251 seqs, 160854530 residues

Total number of hits satisfying chosen parameters: 1009251

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	730	96.4	137	11	Sequence 15, Appl
3	713	94.2	144	11	Sequence 4, Appl
4	658	86.9	121	11	Sequence 2, Appl
5	635	83.9	180	11	Sequence 9, Appl
6	615	81.2	464	14	Sequence 19, Appl
7	615	81.2	464	18	Sequence 9, Appl
8	615	81.2	464	18	Sequence 9, Appl
9	589	77.8	140	8	Sequence 24, Appl
10	583	77.0	143	10	Sequence 26, Appl

11	583	77.0	143	11	US-08-779-784-26	Sequence 26, Appl
12	583	77.0	143	17	US-09-322-862-26	Sequence 26, Appl
13	582	76.9	466	20	US-09-898-705-11	Sequence 11, Appl
14	572	75.6	121	11	US-08-700-737-55	Sequence 55, Appl
15	567	74.9	470	18	US-09-408-646-143	Sequence 143, Appl
16	567	74.9	470	18	US-09-499-662-143	Sequence 143, Appl
17	565	74.6	470	18	US-09-408-646-145	Sequence 145, Appl
18	565	74.6	470	18	US-09-499-662-145	Sequence 145, Appl
19	564	74.5	470	14	US-09-053-583-117	Sequence 117, Appl
20	564	74.5	470	18	US-09-408-646-117	Sequence 117, Appl
21	564	74.5	470	18	US-09-408-646-147	Sequence 147, Appl
22	564	74.5	470	18	US-09-499-662-117	Sequence 117, Appl
23	564	74.5	470	18	US-09-499-662-147	Sequence 147, Appl
24	556	73.4	145	14	US-09-053-583-75	Sequence 75, Appl
25	556	73.4	145	18	US-09-408-646-75	Sequence 75, Appl
26	556	73.4	145	18	US-09-499-662-75	Sequence 75, Appl
27	556	73.4	470	14	US-09-053-583-89	Sequence 89, Appl
28	556	73.4	470	18	US-09-408-646-89	Sequence 89, Appl
29	556	73.4	470	18	US-09-499-662-89	Sequence 89, Appl
30	549	72.5	140	8	US-08-475-815-11	Sequence 11, Appl
31	549	72.5	140	13	US-08-921-060-11	Sequence 11, Appl
32	549	72.5	137	12	US-09-238-741-4	Sequence 4, Appl
33	548.5	72.5	470	18	US-08-864-983A-21	Sequence 21, Appl
34	545	72.0	470	18	US-09-408-646-157	Sequence 157, Appl
35	545	72.0	470	18	US-09-499-662-157	Sequence 157, Appl
36	544.5	71.9	139	5	US-08-137-117B-35	Sequence 35, Appl
37	544.5	71.9	139	5	US-08-137-117C-35	Sequence 35, Appl
38	544.5	71.9	139	15	US-09-114-285-35	Sequence 35, Appl
39	544.5	71.9	139	15	US-09-114-285A-35	Sequence 35, Appl
40	541	71.5	140	8	US-08-475-813-6	Sequence 6, Appl
41	536	70.8	119	4	US-08-073-967-44	Sequence 44, Appl
42	536	70.8	119	9	US-08-553-497-12	Sequence 12, Appl
43	532	70.3	138	6	US-08-286-754-78	Sequence 78, Appl
44	532	70.3	138	8	US-08-408-724-78	Sequence 78, Appl
45	532	70.3	138	21	US-09-753-436-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1

US-08-700-737-15
; Sequence 15, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Tarran
; APPLICANT: Newman, Walter
; APPLICANT: Saldanha, Jos
; APPLICANT: Bendig, Mary M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
; TITLE OF INVENTION: INTEGRIN
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,737
; FILING DATE: 15-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS95-i0

US-08-700-737-4

US-08-700-737-2

67 IGEIDPESNTNYNQFKGKATLTVDISSRAYMQLSLTSDESAVYCYCARGGYDWDYA 12

Db 67 IGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWYA 126
 QY 127 IDYWGQGTSTVTSS 140
 Db 127 IDYWGQGTSTVTSS 140

RESULT 4
 US-08-700-737-9
 ; Sequence 9, Application US/08700737
 ; GENERAL INFORMATION:
 ; APPLICANT: Ponath, Paul D.
 ; APPLICANT: Ringler, Douglas J.
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Saldanha, Jos
 ; APPLICANT: Bendig, Mary M.
 ; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700.737
 ; FILING DATE: 15-AUG-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBER: LKS95-10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 121 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-700-737-9

Query Match 86.9%; Score 658; DB 11; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.2e-55;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 QVQLQPGAEVLKPGTSTVKLSCKGKGYTFTSYMMHWKQRPQGQLEWIGETIDPSESNTNY 79
 Db 1 QVQLQPGAEVLKPGTSTVKLSCKGKGYTFTSYMMHWKQRPQGQLEWIGETIDPSESNTNY 60
 QY 80 NQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWYDAIDYWGQGTSTVTS 139
 Db 61 NQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWYDAIDYWGQGTSTVTS 120
 QY 140 S 140
 Db 121 S 121

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 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 QVQLQPGAEVLKPGTSTVKLSCKGKGYTFTSYMMHWKQRPQGQLEWIGETIDPSESNTNY 79
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 QY 80 NQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWYDAIDYWGQGTSTVTS 139
 Db 61 NQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWYDAIDYWGQGTSTVTS 120
 QY 140 S 140
 Db 121 S 121

RESULT 5
 US-08-700-737-19
 ; Sequence 19, Application US/08700737
 ; GENERAL INFORMATION:

; APPLICANT: Ponath, Paul D.
 ; APPLICANT: Ringler, Douglas J.
 ; APPLICANT: Jones, S. Tarran
 ; APPLICANT: Newman, Walter
 ; APPLICANT: Saldanha, Jos
 ; APPLICANT: Bendig, Mary M.
 ; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH '4 7
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700.737
 ; FILING DATE: 15-AUG-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBER: LKS95-10
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 180 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-700-737-19

Query Match 83.9%; Score 635; DB 11; Length 180;
 Best Local Similarity 86.7%; Pred. No. 3.1e-53;
 Matches 117; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 6 IILFLVSTATSVHSQVQLQPGAEVLKPGTSTVKLSCKGKGYTFTSYMMHWKQRPQGQLE 65
 Db 6 VILFLVSTATSVHSQVQLQPGAEVLKPGTSTVKLSCKGKGYTFTSYMMHWKQRPQGQLE 65
 QY 66 WIGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWY 125
 Db 66 WIGEIDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSLTSEDSAVYVCARGYDGDWY 125
 QY 126 AIDYWGQGTSTVTSS 140
 Db 126 AIDYWGQGTSTVTSS 140

RESULT 6
 US-09-053-583-9
 ; Sequence 9, Application US/09053583A
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, Nobufusa
 ; APPLICANT: Ichikawa, Kimihisa
 ; APPLICANT: Ohtsumi, Jun
 ; APPLICANT: Ohtsuki, Masahiko
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Takahashi, Tohru
 ; APPLICANT: Yoshida, Hiroko
 ; APPLICANT: Shiraiishi, Akio
 ; APPLICANT: Yonehara, Shin
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126/HG

Sat Apr 14 08:10:23 2001

```

; CURRENT APPLICATION NUMBER: US/09/053.583A
; CURRENT FILING DATE: 1998-04-01
; EARLIER APPLICATION NUMBER: JP HEI 9-82953
; EARLIER FILING DATE: 1997-04-01
; EARLIER APPLICATION NUMBER: JP HEI 9-169088
; EARLIER FILING DATE: 1997-06-25
; EARLIER APPLICATION NUMBER: JP HEI 9-276064
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-053-583-9

Query Match      81.2%; Score 615; DB 14; Length 464;
Best Local Similarity 84.3%; Pred. No. 7.8e-51;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPAGAEVLKPGTSVKLSCKGCGYGTFTSYMMHWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSCIILFLVATATGVHSQVLOQPAGAEVLKPGASVKLSCKRAGSYGTFTSYMMQWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GQGLEWIG:IDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGY 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLEWIG:IDPDSYNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 DGWDYADYWGOGTSVTSS 140
   :: ||||| |||||
Db 121 YSNWYF:WVGTTGTTVTSS 140
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RESULT 7
US-09-408-646-9
; Sequence 9, Application US/09408646A
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 990540/HG
; CURRENT APPLICATION NUMBER: US/09/408,646A
; CURRENT FILING DATE: 1999-09-30
; EARLIER APPLICATION NUMBER: JP 10-276881
; EARLIER FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-408-646-9

Query Match      81.2%; Score 615; DB 18; Length 464;
Best Local Similarity 84.3%; Pred. No. 7.8e-51;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPAGAEVLKPGTSVKLSCKGCGYGTFTSYMMHWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSCIILFLVATATGVHSQVLOQPAGAEVLKPGASVKLSCKRAGSYGTFTSYMMQWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GQGLEWIG:IDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGY 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLEWIG:IDPDSYNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 DGWDYADYWGOGTSVTSS 140
   :: ||||| |||||
Db 121 YSNWYF:WVGTTGTTVTSS 140
   :: ||||| |||||

RESULT 9
US-08-487-165-24
; Sequence 24, Application US/08487165
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,165
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA: US 07/946,421
; APPLICATION NUMBER:
; FILING DATE: 06-NOV-1992
; PRIOR APPLICATION DATA: WO PCT/EP92/00480
; APPLICATION NUMBER:
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
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RESULT 8
US-09-499-662-9
; Sequence 9, Application US/09499662
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/09/499,662
; CURRENT FILING DATE: 2000-02-09
; EARLIER APPLICATION NUMBER: US 09/053,583
; EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-499-662-9

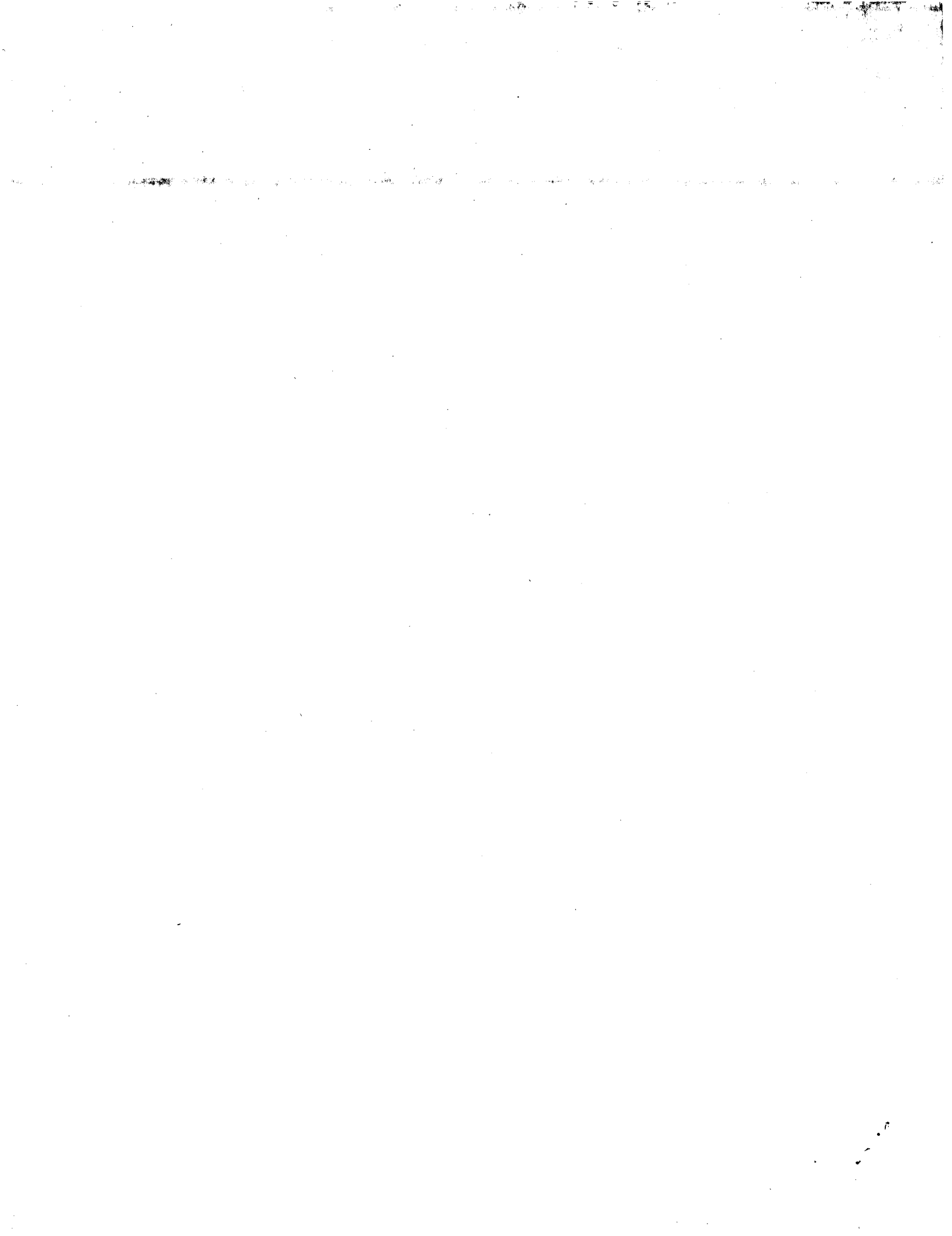
Query Match      81.2%; Score 615; DB 18; Length 464;
Best Local Similarity 84.3%; Pred. No. 7.8e-51;
Matches 118; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPAGAEVLKPGTSVKLSCKGCGYGTFTSYMMHWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSCIILFLVATATGVHSQVLOQPAGAEVLKPGASVKLSCKRAGSYGTFTSYMMQWVKORP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GQGLEWIG:IDPSESNTYNNQKFKGKATLTVDISSSTAYMQLSSLTSEDSAVVYCARGY 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLEWIG:IDPDSYNTYNNQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVVYCARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 DGWDYADYWGOGTSVTSS 140
   :: ||||| |||||
Db 121 YSNWYF:WVGTTGTTVTSS 140
   :: ||||| |||||

RESULT 9
US-08-487-165-24
; Sequence 24, Application US/08487165
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,165
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA: US 07/946,421
; APPLICATION NUMBER:
; FILING DATE: 06-NOV-1992
; PRIOR APPLICATION DATA: WO PCT/EP92/00480
; APPLICATION NUMBER:
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
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RESULT 10
US-08-692-084-26
; Sequence 26, Application US/08692084
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM REMYELINATION USING MONOC
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/692,084
; FILING DATE: 08-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:

RESULT 11
US-08-779-784-26
; Sequence 26, Application US/08779784
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: /US/08/779,784
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/692,084
; FILING DATE: 08-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,520
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-779-784-26



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 17:37:56 ; Search time 4.45 Seconds
(without alignments)
54.611 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHSO.....DGWDYALDYGQGTSTVTSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7695 seqs, 1735856 residues

Total number of hits satisfying chosen parameters: 7695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	549	72.5	140	4	US-08-475-815A-11
2	463	61.2	132	5	US-09-386-658-2
3	282.5	37.3	482	5	US-09-509-031-16
4	242	32.0	240	5	US-09-782-504-4
5	122	16.1	128	4	US-08-475-815A-7
6	107	14.1	155	5	US-09-509-031-11
7	107	14.1	342	5	US-09-509-031-6
8	107	14.1	495	5	US-09-509-031-4
9	69.5	9.2	442	5	US-09-739-449-9534
10	66.5	8.8	914	5	US-09-193-562D-28
11	65	8.6	517	5	US-09-739-449-12328
12	65	8.6	753	1	PCT-US01-09226-51
13	64	8.5	281	5	US-09-739-449-11638
14	63.5	8.4	170	5	US-09-814-950-4
15	63.5	8.4	172	5	US-09-814-950-2
16	62.5	8.3	109	5	US-09-386-658-4
17	62	8.2	757	5	US-09-739-449-11939
18	60.5	8.0	1008	5	US-09-308-453-2
19	60	7.9	240	5	US-09-739-449-12522
20	59.5	7.9	317	5	US-09-706-029-1
21	59.5	7.9	639	5	US-09-739-449-11223
22	59	7.8	574	5	US-09-815-108-7
23	58.5	7.7	342	5	US-09-815-108-20
24	58.5	7.7	379	5	US-09-813-408-6
25	58.5	7.7	448	5	US-09-815-108-6
26	58.5	7.7	472	5	US-09-815-108-5
27	58.5	7.7	504	5	US-09-815-108-8

28 58.5 7.7 504 5 US-09-815-108-15
29 58.5 7.7 504 5 US-09-815-108-17
30 58.5 7.7 504 5 US-09-815-108-19
31 58.5 7.7 509 5 US-09-815-108-3
32 58.5 7.7 529 5 US-09-815-108-2
33 58.5 7.7 594 5 US-09-815-108-22
34 57.5 7.6 418 5 US-09-739-449-10479
35 57.5 7.6 1112 5 US-09-739-449-10300
36 57 7.5 251 5 US-09-739-449-12898
37 56.5 7.5 172 5 US-09-810-264-26
38 56.5 7.5 322 5 US-09-739-449-8302
39 56 7.4 652 5 US-09-813-742-5
40 56 7.4 1144 5 US-09-813-742-3
41 55.5 7.3 215 5 US-09-739-449-10936
42 55.5 7.3 571 5 US-09-809-391-481
43 55.5 7.3 1758 5 US-09-739-449-11627
44 55 7.3 101 5 US-09-809-391-754
45 55 7.3 216 5 US-09-739-449-12644

ALIGNMENTS

RESULT 1
US-08-475-815A-11
; Sequence 11, Application US/08475815A
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; APPLICANT: Rastetter, William H.
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
; TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY WINTHROP
; STREET: 1100 New York Avenue, N.W., Ninth FL.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,815A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,099
; FILING DATE: 03-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,891
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 23522-0157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-815A-11

Sequence 15, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 10479, A
Sequence 10300, A
Sequence 12898, A
Sequence 26, Appl
Sequence 8302, Ap
Sequence 5, Appl
Sequence 3, Appl
Sequence 10936, A
Sequence 481, App
Sequence 11627, A
Sequence 734, App
Sequence 12644, A


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RESULT      7
US-09-509-031-6
; Sequence 6, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koenigen, Frank
; APPLICANT: Suess, Gabriele M.
; APPLICANT: Tarlington, David M.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TLHL protein
; OTHER INFORMATION: sequence
US-09-509-031-6

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Query Match      14.1%; Score 107; DB 5; Length 155;
Best Local Similarity 27.3%; Pred. No. 3e-05;
Matches 35; Conservative 19; Mismatches 46; Indels 28; Gaps

QY 21 VOLQOQCAELVKGCTSVKLSCKG-----YGYFTSTVMHWVQRPQCG---LEWIGEID 71
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 32 VMTQSPDSLAVSLGERATINCKSSQVLYSSNSKNY-LAWYQKQGPQPKLLIYW----- 85
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QY 72 PSESNTNYNKGKFGKATLTVDISSSTAYVQLSLSLTSSEDSAVVYCARGGYGDMDYATDY-W 130
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Db 86 ASTRESQVDPFSSG-----SGTDFTLTISLQAEADVAVVYCOQ-----YYSTPYSF 133
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 131 GQGTSTVTV 138
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Db 134 GQGTKLEI 141
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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9534

Query Match          9.2%; Score 69.5; DB 5; Length 442;
Best Local Similarity 25.0%; Pred. No. 0.72;
Matches 30; Conservative 11; Mismatches 50; Indels 29; Gaps 6;

QY 21 VOLQOPG/ELVKPGTSVKLSCKG-----XYTFTSYMMHWKORPGQ-----LEWIGEID 71
DB 32 VMTQSPD/LAVSLGERATINCKSSQSVLYSSSKNY-LAWYQKPGQPPKLLIYW-----85

QY 72 PSESTN'NOKFKGKATLTVDISSTAYMOLSSLTSEDSAVYCYARGGYDGDWYAIIDY-W 130
DB 86 ASTRESGVPDRFSGS-----SGTDFTLTSSLQAEADVAVYVCOQ-----YVSTPYSF 133

QY 131 GQGTSTVTV 138
DB 134 GQGTKLEI 141

RESULT 8
US-09-509-031-4
; Sequence 4, Application US/09509031
; GENERAL INFORMATION:
; APPLICANT: Koeltgen, Frank
; APPLICANT: Swass, Gabriele M.
; APPLICANT: Ta-linton, David M.
; APPLICANT: Trautlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBIOTIDES AND A METHOD OF PRODUCING SAME
; FILE REFERENCE: 13474
; CURRENT APPLICATION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CATAB-TEV
US-09-509-031-4

Query Match          14.1%; Score 107; DB 5; Length 495;
Best Local Similarity 27.3%; Pred. No. 0.00011;
Matches 35; Conservative 19; Mismatches 46; Indels 28; Gaps 7;

QY 21 VOLQOPG/ELVKPGTSVKLSCKG-----XYTFTSYMMHWKORPGQ-----LEWIGEID 71
DB 32 VMTQSPD/LAVSLGERATINCKSSQSVLYSSSKNY-LAWYQKPGQPPKLLIYW-----85

QY 72 PSESTN'NOKFKGKATLTVDISSTAYMOLSSLTSEDSAVYCYARGGYDGDWYAIIDY-W 130
DB 86 ASTRESGVPDRFSGS-----SGTDFTLTSSLQAEADVAVYVCOQ-----YVSTPYSF 133

QY 131 GQGTSTVTV 138
DB 134 GQGTKLEI 141

RESULT 9
US-09-739-449-9534
; Sequence 9534, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Steven J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9534
```

```
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9534

Query Match          9.2%; Score 69.5; DB 5; Length 442;
Best Local Similarity 25.0%; Pred. No. 0.72;
Matches 30; Conservative 11; Mismatches 50; Indels 29; Gaps 6;

QY 28 AELVPGTSVKLSCKGXYTFTSYMMHWKORPGQGLEWI--GEIDPSESNTN'NQKFKG 85
DB 97 AILPOPLADLAARGLVPLGDDTAKWYEENYGAKSVWDLGSKYKGDGNKAY-FAPFF 155

QY 86 KATLTVDISSTAYM-----QLSSLTSE---DSAVYCY---ARGGYDGW 123
DB 156 KA-----DVKSLVWYVPENFEAGYKVPESMEDLLKLTQDIDVADGGTPWCIGLGGSGATGW 211

RESULT 10
US-09-193-562D-28
; Sequence 28, Application US/09193562D
; GENERAL INFORMATION:
; APPLICANT: Paull, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
; FILE REFERENCE: 18617.0052
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 28
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-562D-28

Query Match          8.8%; Score 66.5; DB 5; Length 914;
Best Local Similarity 25.0%; Pred. No. 3.4;
Matches 34; Conservative 17; Mismatches 50; Indels 35; Gaps 7;

QY 11 VSTATSVHSQ-VLOQOPGAELVKP-----GTSVKLSCKGXYTFTSYMMHWKORPGQGL 64
DB 475 LSSGNGAVSORSIQLESKGLTQNSQWMNGTVIVDSVCKDTFLITW-----TTQPPQIL 530

QY 65 EWIGEIDPSESNTN'NQKFKGKATLTVDISSTAYMOLSSLTSEDSAVYCYARGGYDGDW 124
DB 531 LW-----DPS-----GQKQGG---FVVDKNTKWAYLIQPIAKVGT-----WK 565

QY 125 YAIIDYWGQGTSTVTVSS 140
DB 566 YSLQASSQTLLTAVTS 581

RESULT 11
US-09-739-449-12328
; Sequence 12328, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)C
; CURRENT APPLICATION NUMBER: US/09/739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 12328
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
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US-09-739-449-12328

Query Match
Best Local Similarity 8.6%; Score 65; DB 5; Length 517;
Matches 41; Conservative 22; Mismatches 41; Indels 62; Gaps 14;
QY 12 STATSVH--SOVLOQPGAEVLKPGT--SVKLSCK-----GYGTFSTSYW-----HWK 57
DB 365 SDAASVGAALWVLFQSAK-----ATGIDLGKREPDDGY---NSNVWKKKPFVCVSYW-N 416
QY 58 QRP-----GQGLEWGEIDPSNTNYNQKFKG---KATLTVDIS--SSTAYMOLS 103
DB 417 GRPTEDDMFSLYAKGVDM-----NESHWD-NERFNSLLVKARTTLDEKLAEMYHEMQ 469
QY 104 SLTSDSA-----VYV-----CARGG-----YDGMVDAIDYV 130
DB 470 GLVSEGGTIIPIPVFNVDVNDKVAHGVPVANNRFFDGGKIVRWW 515

RESULT 12
PCT-US01-09226-51
; Sequence 51, Application PC/TUS0109226
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: PCT/US01/09226
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-09226-51

Query Match
Best Local Similarity 8.6%; Score 65; DB 1; Length 753;
Matches 21; Conservative 15; Mismatches 33; Indels 16; Gaps 3;
QY 20 QVLOQPGAEVLKPGT-----SVKLSCKGYGTFSTSYWVHKQRPQGLEWIGE 70
DB 57 RVEIQRAG-----EWGTCDDDDFTLQAAILCLRELGTGTEATGWTSAKYVPGTGRILNDL 112
QY 71 DPS---ESNTNYNQKFKGKATLTVD 92
DB 113 SCSTGEQSVTECASRGWNSDCTHD 137

RESULT 13
US-09-739-449-11638
; Sequence 11638, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10/15490/C
; CURRENT APPLICATION NUMBER: US/09739,449
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 11638
; LENGTH: 281

; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-11638
Query Match
Best Local Similarity 8.5%; Score 64; DB 5; Length 281;
Matches 23; Conservative 17; Mismatches 35; Indels 14; Gaps 4;
QY 43 GYGTFSTSYWVHKQRPQGLEWIGEIDPSNTNYNQKFKGKATLTVDISSTAYMOL 102
DB 90 GVGYGTFSTSYWVHKQRPQGLEWIGEIDPSNTNYNQKFKGKATLTVDISSTAYMOL 142
QY 103 SS-----LTSEDSAVYCA---RGYDGDWD 124
DB 143 ANAYVDLTGYGTSITPYVGGGIGGSYVKWD 171

RESULT 14
US-09-814-950-4
; Sequence 4, Application US/09814950
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Human
US-09-814-950-4

Query Match
Best Local Similarity 8.4%; Score 63.5; DB 5; Length 170;
Matches 20; Conservative 11; Mismatches 37; Indels 29; Gaps 1;
QY 19 SOVLOQPGAEVLKPGT--SVKLSCKGYGTFSTSYWVHKQRPQGLEWIGEIDPSNTN 78
DB 59 TKYQISQPEVYVAAPGESLEVRCLLKDAVISWTKDGVHLGNPNTVLIGE----- 109
QY 79 YNQKFKGKATLTVDISSTAYMQLSSLTSEDSAVYVC 115
DB 110 -----YLOIKGATPRDSGLYAC 126

RESULT 15
US-09-814-950-2
; Sequence 2, Application US/09814950
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01174
; CURRENT APPLICATION NUMBER: US/09/814,950
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human
US-09-814-950-2

Query Match
Best Local Similarity 8.4%; Score 63.5; DB 5; Length 172;
Matches 20; Conservative 11; Mismatches 37; Indels 29; Gaps 1;

	Matches	20; Conservative	11; Mismatches	37; Indels	29; Gaps	1;
Qy	19	SOVQLQIQIGAEIVKPGCTSVKLSCKGYGTYFTSYWVHWKORPGQGLEWIGEDIPSESNTN	78			
Db	59	TKYQISQIEVYVAAPGESLEVRCLLKDAKRAVISWTKDGVHLGPNRTVLIGE	109			
Qy	79	YNQKFKGIATLTVDISSSTAYMQLSSLTSEDSAVYYC	115			
Db	110	-----YLIQKGATPRDSGLYAC	126			

Search completed: April 13, 2001, 17:37:57
Job time: 173 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 13, 2001, 15:36:11 ; Search time 28.17 seconds
(without alignments)
95.475 Million cell updates/sec

Title: US-08-700-737-15
Perfect score: 757
Sequence: 1 MGWSCIILFLVSTATSVHQS.....DGWDYDIDYWGQTSVTSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PTDUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	78.9	464	1	US-08-353-400-36
2	589	77.8	140	1	US-07-946-421-24
3	583	77.0	143	1	US-08-236-520-7
4	583	77.0	143	5	PCT-US95-05262-7
5	544.5	71.9	139	1	US-08-137-117D-35
6	544.5	71.9	139	2	US-08-436-717-35
7	541	71.5	140	1	US-08-476-275-6
8	536	70.8	119	2	US-08-553-497A-12
9	532	70.3	138	1	US-08-482-882-78
10	532	70.3	138	2	US-08-483-389-78
11	532	70.3	138	2	US-08-487-113D-78
12	532	70.3	138	2	US-08-473-503-78
13	532	70.3	138	2	US-08-483-932-78
14	532	70.3	138	2	US-08-720-420A-78
15	532	70.3	138	3	US-08-714-017-78
16	532	70.3	138	3	US-08-475-680-78
17	531	70.1	136	5	PCT-US93-11611-4
18	527.5	69.7	139	1	US-08-253-877C-8
19	527.5	69.7	139	2	US-08-452-164A-8
20	526.5	69.6	138	3	US-08-603-024-2
21	524	69.2	119	3	US-08-881-037-62
22	521.5	68.9	269	2	US-08-428-257A-72
23	521.5	68.9	269	2	US-08-491-988-3
24	521.5	68.9	402	2	US-08-491-988-9
25	521.5	68.9	415	2	US-08-491-988-7
26	521.5	68.9	435	2	US-08-491-988-5
27	520.5	68.8	122	1	US-08-236-520-9

28	520.5	68.8	122	5	PCT-US95-05262-9	Sequence 9, Appl
29	520	68.7	119	2	US-08-553-497A-8	Sequence 8, Appl
30	517	68.3	445	1	US-08-353-400-33	Sequence 33, Appl
31	517	68.3	119	3	US-08-881-037-61	Sequence 61, Appl
32	516	68.2	119	3	US-08-881-037-63	Sequence 63, Appl
33	516	68.2	136	5	PCT-US93-11611-11	Sequence 11, Appl
34	516	68.2	468	2	US-08-303-569B-7	Sequence 7, Appl
35	516	68.2	468	2	US-08-116-247-7	Sequence 7, Appl
36	515.5	68.1	151	4	US-08-513-968-34	Sequence 34, Appl
37	515	68.0	140	4	US-08-579-378A-12	Sequence 12, Appl
38	515	68.0	140	5	PCT-US93-11612-12	Sequence 12, Appl
39	515	68.0	152	1	US-07-634-278-101	Sequence 101, App
40	515	68.0	152	1	US-08-477-728-101	Sequence 101, App
41	515	68.0	152	1	US-08-474-040-101	Sequence 101, App
42	515	68.0	152	1	US-08-487-200-101	Sequence 101, App
43	515	68.0	152	4	US-08-484-537-101	Sequence 101, App
44	513	67.8	119	3	US-08-881-037-60	Sequence 60, Appl
45	513	67.8	119	4	US-08-767-128-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-353-400-36
; Sequence 36, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/08/353,400
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-36

Query Match 78.9%; Score 597; DB 1; Length 464;
Best Local Similarity 80.0%; Pred. No. 3e-47;
Matches 112; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY	1	MGWSCIILFLVSTATSVHQS	QVQLQPGAEIVKPTSVKLSCGKGYTFTSYNMHWKQRP	60
DB	1	MGWSCIILFLVATGTDVHSQVQLQPGAEIVKPGASVQLSCKASGTYFTGYIHWKQRP	60	
QY	61	GGGLEWIGEIDPESNTNYNQKPKKATITVDISSSTAYMQLSSLTSEDSAVVYCARGY	120	
DB	61	GGGLEWIGEIVNFTSGRSDYNEKFKKATITVDKSSSTAYMQLSSLTSEDSAVVYCARERA	120	
QY	121	DGWDYDIDYWGQTSVTSS	140	
DB	121	YGDDAMDYWGQTSVTSS	140	

Matches	113;	Conservative	6;	Mismatches	21;	Indels	0;	Gaps	0;
QY	1	MGWSCIIIFLVSTATSVHSGVQLQQPGCAELVPKCTSVKLSCCKGYGTYFTSYWMHWVKORP	60						
DDB	1	MGWSIILFLVATATDVHSQVQLQQPGCAELVPKGASVKLSCRAGYTFTSHMHWVKORA	60						
QY	61	GGGLEWIEIDPSSENNTNNYNOKFKRATLTVDLISSSTAYMYQLSSLTSEDSAVYYCARGY	120						
Db	61	GGGLEWIIEFNPNSGRNTNNEKFKSATLTVDKSSSTAYMYQLSSLTSEDSAVYYCASRDY	120						
QY	121	DGWDAIAIDYGQGQTSTVTSSS	140						
Ddb	121	DYDGRFYDWGQGTTLATVSS	140						
RESULT 3									
US-08-236-520-7									
; Sequence 7, Application US/08236520									
; Patent No. 5591629									
; GENERAL INFORMATION:									
; APPLICANT: Rodriguez, Moses									
; APPLICANT: Miller, David J.									

```

1  RESULT      6
2  US-08-436-717-35
3  ; Sequence 35, Application US/08436717
4  ; Patent No. 5817790
5  ; GENERAL INFORMATION:
6  ; APPLICANT: TSUCHIYA, Masayuki
7  ; APPLICANT: SATO, Koh
8  ; APPLICANT: BENDIG, Mary
9  ; APPLICANT: JONES, Steven
10 ; APPLICANT: SALDANHA, Jose
11 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
12 ; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
13 ; NUMBER OF SEQUENCES: 158
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: Foley & Lardner
16 ; STREET: 3000 K Street, N.W., Suite 500
17 ; CITY: Washington
18 ; STATE: D.C.
19 ; COUNTRY: USA
20 ; ZIP: 20007-5109
21 ; COMPUTER READABLE FORM:
22 ; MEDIUM TYPE: Floppy disk
23 ; COMPUTER: IBM PC compatible
24 ; OPERATING SYSTEM: PC-DOS/MS-DOS
25 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
26 ; CURRENT APPLICATION DATA:
27 ; APPLICATION NUMBER: US/08/436,717
28 ; FILING DATE:
29 ; CLASSIFICATION: 536
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: US/08/137,117
32 ; FILING DATE: 20-DEC-1993
33 ; APPLICATION NUMBER: WO PCT/JF92/00544
34 ; FILING DATE: 24-APR-1992
35 ; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGIER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: 202)672-5399
TELEX: 90,136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-35

Query Match 71.9%; Score 544.5; DB 2; Length 139;
Best Local Similarity 72.9%; Pred. No. 4.7e-43;
Matches 102; Conservative 13; Mismatches 24; Indels 1; Gaps 1;
QY 1 MGWSCILFLVSTATSVHSGVQLQPGAEVLKPKGTSVKLSCKGCGYGTFTSYNHHWVKQRP 60
DB 1 MGWSGVFLVLSVTAGVHSGVQLQPGAEVLKPKGTSVKLSCKGCGYGTFTSYNHHWVKQRP 60
QY 61 GQGLEWIGETIDPSESNTNNOKEFGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
DB 61 GHGLEWIGETIDPSESNTNNOKEFGKATLTVDISSSTAYMQLSSLTSEDSAVYYCASLDS 120
QY 121 DGWDYALDYWGQGTSTVTVSS 140
DB 121 SGY-YAM)YWGQGTSTVTVSS 139

RESULT 7
US-08-476-275-6
Sequence 6, Application US/08476275
Patent No. 5776156
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Ianna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Lewman, Roland A.
APPLICANT: Reiff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
TITLE OF INVENTION: Lymphoma
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 619 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: JSA
ZIP: 22311
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-275-6

Query Match 71.5%; Score 541; DB 1; Length 140;
Best Local Similarity 75.0%; Pred. No. 9.9e-43;
Matches 105; Conservative 10; Mismatches 25; Indels 0; Gaps 0;
QY 1 MGWSCILFLVSTATSVHSGVQLQPGAEVLKPKGTSVKLSCKGCGYGTFTSYNHHWVKQRP 60
DB 1 MGWSLILLFLVAVATRVLSQVQLQPGAEVLKAGASVKMSCKAGYGTFTSYNHHWVKQTP 60
QY 61 GQGLEWIGETIDPSESNTNNOKEFGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGGY 120
DB 61 GRGLEWIGAIYPGNGDTSYNOKFGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTY 120
QY 121 DGWDYALDYWGQGTSTVTVSS 140
DB 121 YGGDWYFNWAGCTTTVTSA 140

RESULT 8
US-08-553-497A-12
Sequence 12, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESCA
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-12

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Query Match 70.8%; Score 536; DB 2; Length 119;
Best Local Similarity 85.1%; Pred. No. 2.3e-42;
Matches 103; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 20 QVLOQPGAEVLKPGTSVKLSCKGYGTYTTSYMMHWKORPGGLEWIGEIDPSESNTNY 79
DB 1 EVLOQSGAEVLKPGASVKLSCKASGYTTSYMMHWKORPGGLEWIGEIDPDSYTN 60
QY 80 NQKFKKATLTVDISSSTAYMQLSSLTSDSAVYYCARGYDGDYDAIDYWGQTSVTVS 139
DB 61 NQKFKKATLTVDKSSSTAYMQLSSLTSDSAVYYCARGYDGDYDAIDYWGQTSVTVS 118
QY 140 S 140
DB 119 S 119

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RESULT 9
US-08-482-882-78
; Sequence 78, Application US/08482882
; Patent No. 5773218
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,882
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5773218and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-482-882-78

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Query Match 70.3%; Score 532; DB 1; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGWSCIILFLVSTATSVHSQVLOQPGAEVLKPGTSVKLSCKGYGTYTTSYMMHWKORP 60
DB 1 MXWSXXFXFLSVTAGVHSQVLOQSGAEVLADPGASVAMSKASGTYTFTVYMMHWKORP 60
QY 61 GQGLEWIGEIDPSESNTNYNOKFKKATLTVDISSSTAYMQLSSLTSDSAVYYCARGY 120
DB 61 GQGLEWIGYINPTDYTEYNORFQDKATLTADKSSSTAYMQLSSLTSDSAVYYCARG- 119
QY 121 DGWDYDAIDYWGQTSVTVS 140
DB 120 -GNSYGLDYGQGTSTVVS 138

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RESULT 10
US-08-483-389-78
; Sequence 78, Application US/08483389
; Patent No. 5811517
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-RELATED PROTEIN
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,389
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993

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Sat Apr 14 08:10:23 2001

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Suh Young J.
; REGISTRATION NUMBER: P-41,337
; REFERENCE/DOCKET NUMBER: 27866/32760
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-389-78

Query Match 70.3%; Score 532; DB 2; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGWSCIIILFVSTATSVHSQVQLQPGAEIVKPGTSVKLSCKGKGYFTFTSYMMHWKQRP 60
Db 1 MXSWXXXFLFSVTAGVHSQVQLQSSAELADPGASVKMSCKASGYFTFTVYMMHWKQRP 60
QY 61 GQGLEWIGEDPSNTNNTNPKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
Db 61 GQGLEWIGYINPNTDYTEYNQRFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARWG- 119
QY 121 DGWDYAIQYWGQGTSTVTVSS 140
Db 120 -GNSYGLDYGQGTSTVTVSS 138

RESULT 11
US-08-487-113D-78
; Sequence 78, Application US/08487113D
; Patent No. 583/822
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 3300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,113D
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
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; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5837822and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-113D-78

Query Match 70.3%; Score 532; DB 2; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGWSCIIILFVSTATSVHSQVQLQPGAEIVKPGTSVKLSCKGKGYFTFTSYMMHWKQRP 60
Db 1 MXSWXXXFLFSVTAGVHSQVQLQSSAELADPGASVKMSCKASGYFTFTVYMMHWKQRP 60
QY 61 GQGLEWIGEDPSNTNNTNPKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
Db 61 GQGLEWIGYINPNTDYTEYNQRFQDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARWG- 119
QY 121 DGWDYAIQYWGQGTSTVTVSS 140
Db 120 -GNSYGLDYGQGTSTVTVSS 138

RESULT 12
US-08-473-503-78
; Sequence 78, Application US/08473503
; Patent No. 5869262
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-420A-78

Query Match 70.3%; Score 532; DB 2; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;
Qy 1 MGNWCILFLVSTATSVHVSQVLOQPGAEIVKPGTSVKLSCKGYGTYFTSYNMHWKQRP 60
Db 1 MGNWCILFLVSTATSVHVSQVLOQPGAEIVKPGTSVKLSCKGYGTYFTSYNMHWKQRP 60
Qy 61 GQGLEWIEIDPSESNTNNGKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
Db 61 GQGLEWIEIDPSESNTNNGKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
Qy 121 DGWDYAIQWQGTSTVSS 140
Db 120 -GNSYGLDYWGQGTSTVSS 138

RESULT 15
US-08-714-017-78
Sequence 78, Application US/08714017
Patent No. 604C176
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6040176and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-714-017-78

Query Match 70.3%; Score 532; DB 3; Length 138;
Best Local Similarity 73.6%; Pred. No. 6.5e-42;
Matches 103; Conservative 6; Mismatches 29; Indels 2; Gaps 1;
Qy 1 MGNWCILFLVSTATSVHVSQVLOQPGAEIVKPGTSVKLSCKGYGTYFTSYNMHWKQRP 60
Db 1 MGNWCILFLVSTATSVHVSQVLOQPGAEIVKPGTSVKLSCKGYGTYFTSYNMHWKQRP 60
Qy 61 GQGLEWIEIDPSESNTNNGKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
Db 61 GQGLEWIEIDPSESNTNNGKFKGKATLTVDISSSTAYMQLSSLTSEDSAVYYCARGY 120
Qy 121 DGWDYAIQWQGTSTVSS 140
Db 120 -GNSYGLDYWGQGTSTVSS 138

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